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Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                                                                                      Result
No.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Database
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Searched:
    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                 1074
1073
1054
                                                                                                                                                                                                                                                                                                                                                                                 %
Query
Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           March 19, 2003, 14:13:59; Search time 1420 Seconds (without alignments) 32.939 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         671580 seqs, 206047115 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BLOSUM62
Gapop 10.0 , Gapext 0.5
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us-10-006-190-1
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sp_rvirus:*
sp_bacteriap:*
sp_archeap:*
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sp_bacteria:*
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sp_phage:*
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sp_mhc:*
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                     Q9NPB4
Q9DTM5
Q9DTM5
Q95J94
Q95J94
Q9FC01
Q9HC01
Q9HC01
Q9HC05
Q9
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              Q9npb4 h cdna flj1
Q9d7zl mus musculu
Q9dbm5 mus musculu
Q9db57 mus musculu
Q9db57 mus musculu
Q9db57 mus musculu
Q9db74 oryctolagus
Q9d8w6 mus musculu
Q9hc01 homo sapien
Q9hc01 homo sapien
Q9hyqu6 drosophila
Q9fk35 arabidopsis
Q8r7x4 thermoanaer
Q39985 neocallimas
Q39987 mus musculu
Q93886 neocallimas
                                                                                                                                                                                                                                                                                                                                                                               Description
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Q8tcy2 homo sapien	Q8TCY2	4	130	23.1	268
	Q9ZUU1	10	284		271
Q8ue38 agrobacteri	Q8UE38	16	196	•	278.5
7	Q9Y0E7	ഗ	229		280
Q9n9i0 leishmania	Q9N9I0	IJ	269	•	292.5
Q96vq0 neocallimas	Q96VQ0	w	151	25.4	294.5
Q96vq2 piromyces s	Q96VQ2	ω	149		303
_	Q96VQ1	ω	149		305
	052412	N	155		315
Q9fij7 arabidopsis	Q9FIJ7	10	283	٠	319
Q9fyq7 arabidopsis	Q9FYQ7	10	217	•	319.5
Q9p9d2 uncultured	Q9P9D2	۳	216	٠	321
O52411 neisseria m	052411		155		322
O52410 neisseria m	052410		155	•	323
Þ	Q9R452		155		323
_	Q8VYL1		588	28.4	329.5
	Q8RE31		211	٠	m
Q99qc7 haemophilus	Q99QC7		159	•	360
<pre>pyrococ</pre>	Q8U207	17	220	•	362.5
haemoph1	Q9AMQ9	ຎ	159		364
Q99q12 haemophilus	Q99Q12	2	159		364
haemophi	Q99QC4	2	159	•	364
haemophi	Q99QD4	N	159		364
Q99q11 haemophilus	Q99Q11	N	159		364.5
w	Q8TCY3	4	202	•	365
drosophile	Q9W1D0	σ	237		378
Q8trs3 methanosarc	Q8TRS3	17	215		385.5
Q9y0a8 cryptospor1	0	Çī	220	33.9	393
Q9u915 drosophila	Q9U915	5	240	•	398.5

## ALIGNMENTS

RA RA A	RRRA	RA	RA	RA	R 7	RN	RL	RT	RA	RA	RA	RA	RC	RP	RN	o X	8	గి	20	DE	DE	DE	ЭG	DE	DE	DT	DT	ΡŢ	AC	IĐ	RESULT Q9NPB4
SEQUENCE FROM N.A. SEQUENCE FROM N.A. Isogai T., Ota T., F Nishikawa T., Nagai	"NEDO human cDNA sequencing Submitted (FEB-2000) to the	Saito K., Yamamoto J	Tanai H., Kimata M.,	Nishikawa T., Nagai	ISOGAÍ T., Ota T., F	[2]	Submitted (FEB-2000) to the	"NEDO human cDNA sequencing project.";	Nakamura Y., Nagahari K., Masuho Y., Sasaki N.;	Matsunawa H., Ishii	Nishikawa T., Nagai	•	TISSUE-PLACENTA; .	SEQUENCE FROM N.A.	[1]		Mammalia; Eutheria;	Eukaryota; Metazoa;	Homo sapiens (Human).	protein).	to GTP: AMP phosphotr	mitochondrial) (CDN)	clone NT2RP3000359,	phosphotransferase n	CDNA FLJ11089 fis, c	01-MAR-2002 (TrEMBL:	01-OCT-2000 (TrEMBLrel.	01-OCT-2000 (TremBLrel		Q9NPB4 PRELIMINARY;	LT 1 B4
Hayashi K., Sugiyama i K., Sugano S., Shira		Yamamoto J., Wakamatsu A., Nakamura	Kimata M., Watanabe M., Hiraoka S.,	K., Sugano S., Ishi	Hayashi K., Suqiyama		) to the EMBL/GenBan	quencing project.";	ri K., Masuho Y., Sa	S., Kawai Y., Saito	K., Sugano S., Aots	Hayashi K., Suqiyama						Chordata; Craniata;	•		ransferase mitochond	A FLJ14628 fis, clon	highly similar to G	nitochondrial (EC 2.	clone PLACE1005305,	(TrEMBLrel. 20, Last annota	rel. 15, Last sequence update	rel. 15, Created)		NARY; PRT; 227	
Suglyama T., Otsuki T., Suzuki Y., S., Shiratori A., Sudo H.,	project."; EMBL/GenBank/DDBJ databases.		ka S., Ishii S., Kawai Y.,	Nishikawa T., Nagai K., Sugano S., Ishibashi T., Fujimori K.,	ISOQAI T., Ota T., Hayashi K., Suqiyama T., Otsuki T., Suzuki Y., ·		EMBL/GenBank/DDBJ databases.			Matsunawa H., Ishii S., Kawai Y., Saito K., Yamamoto J., Wakamatsu A.,	ıka S., Yos	T., Otsuki T., Suzuki Y.,					i; Hominidae;	Vertebrata; Euteleostomi;			to GTP:AMP phosphotransferase mitochondrial) (Hypothetical 25.6 kDa	e NT2RP2000329, highly similar	clone NT2RP3000359, highly similar to GTP:AMP phosphotransferase	phosphotransferase mitochondrial (EC 2.7.4.10) (CDNA FLJ10691 fis,	CDNA FLJ11089 fis, clone PLACE1005305, highly similar to GTP:AMP	Last annotation update)	ce update)			7 AA.	

Q9may0 oryza sativ

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Best Local S
Matches 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPRO00850; Adenylate_kin.
InterPro; IPRO00623; Shik_kinase.
Pfam; Ppf00406; adenylatekinase; 1.
PRINTS; PRO10094; ADENYLTKNASE.
PRINTS; PR01100; SHIKIMTKNASE.
PRODom; PD000657; Adenylate_kin; 1.
PROSITE; PS00113; ADENYLATE_KINASE; 1.
PROSITE; PS00113; ADENYLATE_KINASE; 1.
PROSITE; PS00113; ADENYLATE_KINASE; 1.
SEQUENCE 227 AA; 25565 MW; 98A0EDF4F1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Strausberg R.;
Submitted (SEP-2001) to the E
-1 SIMILARITY: BELONGS TO TH
EMBL; AKO01951; BAA91196.1; -
EMBL; AKO01553; BAA91753.1; -
EMBL; AKO027534; BAB55183.1; -
EMBL; BC013771; AAH13771.1; -
HSSP; P08760; 2AK3.
                                                                                                                                                      Mus musculus (Mouse).
Eukaryota; Metazoa; C
Mammalia; Eutheria; R
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                  Q9D7z1;
STRAIN-C57BL/6J; TISSUE-STOMACH;
MEDLINE-21085660; PubMed-11217851;
Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii
Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda
Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka
Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito
Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbu
                                                                                                                                                                                                                          01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Adenylate kinase 3 alpha like.
                                                                                                                             SEQUENCE
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"NEDO human cDNA sequencing project.";
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                 AKL3L
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        l Similarity 99.1
225; Conservative
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227 AA; 25565 MW; 98A0EDF4FD9C9CEF
                                                                                                                                                                                                                                                                                               PRELIMINARY;
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                                                                                                                                                                    Chordata;
Rodentia;
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THE ADENYLATE KINASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score
Pred.
                                                                                                                                                                    Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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No. 3
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., Ono Y., Takiguchi S
, Kawai Y., Saito K.,
ari K., Masuho Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         databases
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RESULT
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AC QS
DT 01
DT 01
DT 01
DT 03
DE AC

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Q9DBM5 PRELII
Q9DBM5;
O1-JUN-2001 (TrEM)
O1-JUN-2001 (TrEM)
O1-MAR-2002 (TrEM)
Adenylate kinase:

1 (TrEMBLrel. 17, Cre 1 (TrEMBLrel. 17, Las 2 (TrEMBLrel. 20, Las kinase 3 alpha like.

Last sequence up

Created)

227

AΑ

AKL3L.

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Query Match
Best Local S
Matches 209
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Submitted (MAR-2002) to the EMBL,
-1 - SIMILARITY: BELONGS TO THE AI
EMBL; AK008681; BAB25829.1; -.
EMBL; BC016432; AAH16432.1; -.
EMBL; BC019174; AAH19174.1; -.
EMBL; BC0024871; AAH24871.1; -.
EMBL; BC0024871; AAH24871.1; -.
HSSP; P08760; 2AK3.
MGD; MGI:1860835; AK131.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Interpro; IPR000850; Adenylate_kin.
Interpro; IPR000823; Shik_kinase.
Pfam; pP00406; adenylatekinase; 1.
PRINTS; PR00094; ADENYLTKNASE.
PRINTS; PR01100; SHIKIMTKNASE.
PRODOM; PD000657; Adenylate_kin; 1.
PROSITE; PS00113; ADENYLATE_KINASE; 1
Kinase; Transferase.
SEQUENCE 227 AA; 25426 MW; 6601DF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whitther C., Wilming I Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Strausberg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted
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Strausberg R.;
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EPVLQYYQKKGVLETFSGTETNKIWPHVYSFLQTKVPETTQKASVTP
                                                                                                                IKQRLTARWIHPASGRVYNIEFNPPKTVGIDDLTGEPLIQREDDKPETVIKRLKAYEDQT
                                                                                                                                                                                  DQGKLIPDDVMTRLALHELKTLTQCSWLLDGFPRTLPQAEALDKVYQIDTVINLNVPFEV
                                                                                                                                                                                                                                                                           MGASGRLLRAVIMGAPGSGKGTVSSRITKHFELKHLSSGDLLRQNMLQGTEIGVLAKTFI
                                                                                         IKQRLTARWIHPASGRVYNIEFNPPKTVGIDDLTGEPLIQREDDKPETVIKRLKAYEAQT
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92.1%;
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THE ADENYLATE KINASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                        Score 1078; DI
Pred. NO. 2.4e
7; Mismatches
                                                                                                                                                                                                                                                                                                                                                             7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        6601DF10971DE5AC CRC64;
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2.4e-87;
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Wilming L.,
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RESULT
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RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Arakawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schrimi L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Schrimi L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
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RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchlonni L., Mashina J., Mazazarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y., Storch K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Sin
Matches 208;
                              01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence up
01-MAR-2002 (TrEMBLrel. 20, Last annotation
Adenylate kinase 3 alpha like.
                                                                                                                     Q9DB57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PR00094; ADENYLTKNASE.
PRINTS; PR01100; SHIKIMTKNASE.
PRODOM; PD000657; Adenylate_kin; 1.
PROSITE; PS00113; ADENYLATE_KINASE;
Kinase; Transferase.
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InterPro; IPR000850; Adenylate_kin.
InterPro; IPR000623; Shik_kinase.
Pfam; PF00406; adenylatekinase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Functional annotation of a Nature 409:685-690(2001).
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Mammalia; Eutheria;
                                                                                                      Q9DB57;
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                   AKL3L.
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   musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                      IKQRLTARWIHPASGRVYNIEFNPPKTVGIDDLTGEPLIQREDDKPETVIERLKAYEAQT
                                                                                                                                                                                                                                                                                      IKQRLTARWIHPASGRVYNIEFNPPKTVGIDDLTGEPLIQREDDKPETVIKRLKAYEDQT
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                                                                                                                     PRELIMINARY;
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Pred. No. 5.4e
8; Mismatches
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RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Arakawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
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RA Mynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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Nature 409:685-690(2001).

-i - SIMILARITY: BELONGS TO THE ADENYL.
EMBL; AKO05194; BAB23876.1; -
HSSP; P08760; 2AK3.
HSSP; P08760; 2AK3.
InterPro; IPR000850; Adenylate_kin.
InterPro; IPR000623; Shlk_kinase.
Pfam; PF00406; adenylatekinase; 1.
Q95J94 PRELIMINARY; PRT; 227 AA. Q95J94; Q95J94; Q1-DEC-2001 (TrEMBLrel. 19, Created) Q1-DEC-2001 (TrEMBLrel. 19, Last sequence update) Q1-MAR-2002 (TrEMBLrel. 20, Last annotation update) Adenylate kinase 3. Qryctolagus cuniculus (Rabbit). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eukaryota; Metazoa; Chordata; Leporidae; Oryctolag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PRO0094; ADENYLTKNASE.
PRINTS; PRO1100; SHIKIMTKNASE.
PRODOM; PD0000557; Adenylate_kin; 1.
PROSITE; PS00113; ADENYLATE_KINASE;
Kinase; Transferase.
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DQGKLIPDDVMTRLALHELKNLTQYSWLLDGFPRTLPQAEALDRAYQIDTVINLNVPFEV 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25427 MW;
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Pred. No. 6.6e-87;
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                                          Euteleostom1;
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RX STRAIN-C57BL/GJ; TISSUE-PANCREAS;
RX MEDLINE-21085660; PubMed-11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Kondo S., Yamanaka I.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Coasavant T.,
RA Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schrimi L.M., Staubii F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Schrimi L.M., Staubii F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
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RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Gustincich S., Hill D., Hofmann M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Synshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                          A CONTRACTOR OF THE CONTRACTOR
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Q9D8W6
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Eukaryota; Metazoa; Cl
Mammalia; Eutheria; R
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
10 day old male pancreas cDNA, RIKEN full-length enriched
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-I. SIMILARITY: BELONGS TO THE ADENYLATE KINASE FAMILY. EMBL; AF417508; AAL07503.1;
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Pfam; PF00406; adenylatekinase; 1.
ProDom; PD000657; Adenylate_kin; 1.
PROSITE; PS00113; ADENYLATE_KINASE; UNKNOWN_1.
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MEDLINE-21240235; PubMed-11342145;
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207; Conserv
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Pred. No. 3.2e.
6; Mismatches
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Sciurognathi;
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) conductance in Xenopus oocytes
) from renal proximal tubules."
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Best Local
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Nature 409:685-690(2001).

1 - SIMILARITY: BELONGS TO THE ADENYLATE KINASE FAMILY.
R EMBL; AK007618; BAB23139.1; -.
R HSSP; P08760; 2AK3.
R InterPro; IPR000850; Adenylate_kin.
R InterPro; IPR000623; Shik_kinase.
R InterPro; IPR000623; Shik_kinase.
R Pfam; PF00406; adenylatekinase; 1.
R PFNMTS; PR00100; SHIKIMTKNASE.
R PRINTS; PR01100; SHIKIMTKNASE.
R PRODOM; PD000657; Adenylate_kin; 1.
R PTODOM; PD000657; Adenylate_kin; 1.
R PTODOM; PD000657; Adenylate_kin; 1.
R PTOSITE; PS00113; ADENYLATE_KINASE; 1.
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Best Local
                                                                                                                                                                                                                                                                                                 "A novel gene expressed in human pheochromcytoma."; Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databas -i- SIMILARITY: BELONGS TO THE ADENYLATE KINASE FAMII EMBL; AF183419; AAG09688.1; -
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01-MAR-2001
01-MAR-2002
                                                                                                                                                                            InterPro; IPR000850; Adenylate_kin. Pfam; PF00405; adenylatekinase; 1. PRINTS; PR00094; ADENYLTKNASE. ProDom; PD000657; Adenylate_kin; 1. PROSITS; PS00113; ADENYLATE_KINASE; Kinase; Transferase.
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Mammalia; Eutheria;
                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Transferase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 (TremBLrel. 16,
1 (TremBLrel. 16,
2 (TremBLrel. 20,
                                                                                                                                                             157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   189
                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Human)
                                                                                                                                                          ΑĄ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Α.
                                                                                                                                                          18192 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chordata;
                                                                                        69.7%;
98.7%;
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93.1%;
                                                                                      .78;
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                                                               Score 809; DB
Pred. No. 8.4e
0; Mismatches
                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 899; DB 11,
Pred. No. 1.2e-71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                        F7D36803A8A241A4 CRC64;
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                                                           Db
3.4e-64;
2;
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                                                                                                        Length 157
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                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                               0;
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                                                             Gaps
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MTRLALHELKNLTQYSWLLDGFPRTLPQAEALDRAYQIDTVINLNVPFEVIKQRLTARWI

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                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Sim
Matches 134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9H576;
Q9H576;
Q1-MAR-2001 (TrEMBLrel. 16, Created)
Q1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
Q1-MAR-2002 (TrEMBLrel. 20, Last annotation updat
BA6J24.5 (Adenylate kinase 3 alpha) (Fragment).
                                                                                                     Q9VGU6;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
CG6612 protein (Adenylate kinase isozyme 3).
ADK3 OR DAK3 OR CG6612.
SEQUENCE FROM N.A. STRAIN-BERKELEY; MEDLINE-20196006;
                                                         Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musc
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                           Q9VGU6
                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000850; Adenylate_kin.
Pfam; PF00406; adenylatekinase; 1.
PRINTS; PR00094; ADENYLTKNASE.
ProDom; PD000657; Adenylate_kin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases |- SIMILARITY: BELONGS TO THE ADENYLATE KINASE FAMILY. EMBL, AL136231; CAC12706.1; -. HSSP; P08760; 2AK3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
MCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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                                              NCBI_TaxID=7227;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Kinase;
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                                                                                                                                                                                                                                                                                          DLTGEPLIQREDDKPETVIKRLKAYEDQTKXVLXYYQKKGVLETFSGTETIKIWPYVYAF 211
                                                                                                                                                                                                                                                                                                                                      FPRTLPQAEALDRAYQIDTVINLNVPFEVIKQRLTARWIHPASGRVYNIEFNPPKTVGID 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LQTKVPQRSQKASVTP
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                                                                                                                                                                                                                                                        LQTKVPQRSQKASVTP 227
                                                                                                                                                                                                                                                                              DLTGEPLIQREDDKPETVIKRLKAYEDQTKPVLEYYQKKGVLETFSGTETNKIWPYVYAF
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                                                                                                                                                                                                                                                                                                                                                                         Similarity 98.5
34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                             Transferase.
                                                                                                                                                                                                                                                                                                                                                                                                                       136 AA;
                                                                                                                                                                           PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N.A.
 PubMed-10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                       15707 MW;
                                                                                                                                                                                                                                                                                                                                                                                   60.1%;
98.5%;
                                                                                                                                                                                                                                   136
                                                                                                                                                                                                                                                                                                                                                                    Score 698; DB 4; Lei
Pred. No. 4.4e-54;
Prematches 2;
                                                                                                                                                                                                                                                                                                                                                                         0,
                                                                                                                                                                           PRT;
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                                                                   Brachycera; Muscomorpha;
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RA Ballew R.M., Basu A., An H.-J., Andrews-Franksch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Fosler C., Gabriellan A.E., Carg N.S., Gelbart W.M., Glasser K.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Weil M.-H., Ibegwam C.,
RA Kimmel B.E., Kodira C.D., Kratt C., Kravitz S., Kulp D., Lal Z.,
RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.Y., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Williams S.M., Woodsay T., Morriey K.C., Wu D., Yang S., Yao Q.A.,
RA Yeller E., Spradling A.C., Stapleton M., Strong R., Sun E.,
Ra Yeller E., Spradling A.C., Stapleton M., Zhang G., Zhao Q., Zheng L.,
RA Yeller S.M., Rubin G.M., Venter J.C.,
RT The genome sequence of Drosophila melanogaster.";
RI Cience 287:2185-2195(2000).
                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local
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InterPro; IPR000850; Adenylate_kin.

Pfam; pF00406; adenylatekinase; 1.

PRINTS; PR00094; ADENYLTKNASE;

PRODOm; PD000657; Adenylate_kin; 1.

PROSITE; PS00113; ADENYLATE_KINASE; 1

Kinase; Transferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
--- SIMILARITY: BELONGS TO THE ADENYLATE KINASE FAMILY.
EMBL; AE003689; AAF54578.1; --
EMBL; AB050622; BAB44152.1; --
HSSP; P08760; 2AK3.
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186
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                                                                 TARWIHPASGRVYNIEFNPPKTVGIDDLTGEPLIQREDDKPETVIKRLKAYEDQTKXVLX
                                             KNRWIHAPSGRVYNIGFKNPKVPGKDDVTGEPLMQREDDKPHVVAKRLELYDEVMSPVIA
                                                                                                                                             VPDAIVTKTMLARITEVGNRSYILDGFPRNIAQAEALAAREQIDAVITLDVPHSVIIDRV
                                                                                                                                                                    IPDDVMTRLALHELKNLTQYSWLLDGFPRTLPQAEALDRAYQIDTVINLNVPFEVIKQRL 125
YYQKKGVLETFSGTETNKIWPYVYAFLQTKV 216
                                                                                                                                                                                                                                        KIFRAVIIGAPGSGKGTISELICKNHGCVHISTGDILRQNIIKNTELGKKAKQYIAEGKL
                                                                                                                                                                                                                                                                                                                                         106;
                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                      24145 MW;
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50.2%;
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                                                                                                                                                                                                                                                                                                                                                                                      Score 565;
                                                                                                                                                                                                                                                                                                                                                                  Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                      6AB49A756D23091B CRC64;
                                                                                                                                                                                                                                                                                                                                         Mismatches
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                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                           185
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184

WYEKKGLVATEKGKQTKEIWPMMELFLNDRI

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RESULT 11
QBR7X4
ID 08R7Y
AC QBR7Y
AC QBR7Y
DT 01-UI
DT 01-UI
DT 01-UI
DT 01-UI
OT 01-TI
OS Therri
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RN [1]
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                 Q8R7X4 PRELIMINAKX; ...., Q8R7X4; Q8R7X4; Q8R7X4; Created) 01-JUN-2002 (TrEMBLrel. 21, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Adenylate kinase.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eu
eurosida II, Brassicales; Brassicaceae; Arabidopsis.
                                               Thermoanaerobacter tengcongensis.
Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia; Thermoanaerobacteriales; Thermoanaerobacteriaceae; Thermoanaerobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PR00094; ADENYLTKNASE.
ProDom; PD000657; Adenylate_kin; 1.
PROSITE; PS00113; ADENYLATE_KINASE; 1.
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  NCBI_TaxID=119072; [1]
                                                                                                                              Adenylate kinase and ADK OR TTE2271.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kotani H., Nakamura
Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=98403884; PubMed=9734815; Kotani H., Nakamura Y., Sato S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-COLUMBIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=3702;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 182
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                                                                                                                                                                                                                                                                                                                                                                                                                 215
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EERITGRWIHPSSGRSYHTKFAPPKVPGVDDLTGEPLIQRKDDNADVLRSRLDAFHKQTQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KQRLTARWIHPASGRVYNIEFNPPKTVGIDDLTGEPLIQREDDKPETVIKRLKAYEDQTK 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DVMTRLALHELKN--LTQYSWLLDGFPRTLPQAEALD-----RAYQIDTVINLNVPFEVI 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RLVEIGPPGSGKGTQSPVIKDEFCLCHLSTGDMLRAAVAAKTPLGVKAKEAMDKGELVSD
                                                                                                                                                                                                                                                                                                                                                                                                              PVIDYYAKK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RAVIMGAPGSGKGTVSSRITTHFELKHLSSGDLLRDNMLRGTEIGVLAKAFIDQGKLIPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ch 37.8%;
l Similarity 48.7%;
92; Conservative 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Transferase.
E 248 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                              223
                                                                                                                                                                                                                                                                                                                                                                                                                                                              190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27335 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 439; DB
Pred. No. 7.7e
32; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 10;
7.7e-31;
nes 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ą
                                                                                                                                                                           update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kaneko T., Miyajima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 248;
                                                  Thermoanaerobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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RESULT 12
09398
1D 09398
AC 09398
DT 01-MA
DT 01-MA
DT 01-MA
DT 01-MA
OC NEOCA
OC NEOCA
OC NEOCA
OC NEOCA
CO NE
В
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                                                                                            Query Match
Best Local S
Matches 96
                                                                                                                                                                                                                                                                      Voncken F., Boxma B., Verhagen E., van Wesel R., van der Drift (
A Veenhuis M., Hackstein J., Vogels G.;

T "Evidence for a chimeric origin of chytrid hydrogenosomes.";

Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.

- :- SIMILARITY: BELONGS TO THE ADENYLATE KINASE FAMILY.

EMBL; AJ224658; CAA12055.1; --

RR HSSP; P07170; 1AKY.

RR HSSP; P07170; 1AKY.

RR InterPro; IPR000850; Adenylate_kin.

PFAm; PF00406; adenylate_kin.

PFAm; PF00406; ADENYLTKNASE.

RR PFAm; PR000657; Adenylate_kin; 1.

PROSTIE; PS00113; ADENYLATE_KINASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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Best Local
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STRAIN-MB4T / JCM11007;

MEDLINE-21992816; pubMed=11997336;

Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Ya Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Tan H., Chen R., Wang J., Yu J., Yang H.;

"A complete sequence of T. tengcongensis genome.";

Genome Res. 12:689-700(2002).

EMBL; AE013171; AAM25415.1;

Kinase; Complete proteome.

Kinase; Complete proteome.
                                                                                                                                                                                               Kinase; Transferase
NON_TER 231 2
SEQUENCE 231 AA;
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation updat
Adenylate kinase (EC 2.7.4.3) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                093985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Neocallimasticaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Fungi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=L2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=4757;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Neocallimastix frontalis (Rumen fungus)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HDGAKL2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8 LRAVIMGAPGSGKGTVSSRITTHFELKHLSSGDLLRDNMLRGTEIGVLAKAFIDQGKLIP
                               SARLLRAVIMGAPGSGKGTVSSRITTHFELKHLSSGDLLRDNMLRGTEIGVLAKAFIDQG
  SKNSLRMVIMGPPGSGKGTQAPKVKDTYCICHLATGDMLRAAVKAGTPIGMEAKKIMDAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PLIDYYTKKGILVNIDGNKS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KQRLTARWIHPASGRVYNIEFNPPKTVGIDDLTGEPLIQREDDKPETVIKRLKAYEDQTK 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DDVMTRLALHEL-KNLTQYSWLLDGFPRTLPQAEALD-----RAYQIDTVINLNVPFEVI 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MRVVLLGPPGAGKGTQALKIAKEFDIPHISTGDIFRQNLRDNTELGKLAKEYMDKGLLVP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      85;
                                                                                               96; Conserv
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                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chytridiomycota; Ñ
ae; Neocallimastix.
                                                                                                                                                                                               231
25353 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      37.7%;
42.5%;
                                                                                                                       37.3%;
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Pred. No. 8e-3:
42; Mismatches
                                                                                            Score 433.5; DB 3; Pred. No. 2.1e-30; l; Mismatches 81;
                                                                                                                                                                                                    844B51EB554676A2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Neocallimasticales;
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                                                                                                                                               DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16;
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                                                                                                  Indels
                                                                                                                                               Length
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                                                                                               Gaps
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  65
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RESULT 14
Q9CY37
ID Q9CY3
AC Q9CY3
DT 01-JU
DT 01-JU
DT 01-MA
DE Adeny
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Best Local
                               01-JUN-2001
01-JUN-2001
01-MAR-2002
                                                                                                  Q9CY37;
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Piromyces sp. E2.
Eukaryota; Fungi: Chytridiomycota; Neocallimasticaceae; Piromyces.
Neocallimasticaceae; Piromyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation updat
Adenylate kinase (EC 2.7.4.3) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000850; Adenylate_kin.
Pfam; PF00406; adenylatekinase; 1.
PRINTS; PR00094; ADENYLTKNASE;
ProDom; PD000657; Adenylate_kin; 1.
PROSITE; PS00113; ADENYLATE_KINASE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=73868;
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         Adenylate kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kinase; Transferase.
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093986
093986;
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01-MAY-1999
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PRODOM; PD000657; Adenylate_kin; 1.
PROSITE; PS00113; ADENYLATE_KINASE;
Kinase; Transferase.
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Pfam; PF00406; adenylatekinase; 1.
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  Created)
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RA Kawai J. Shinagawa A. Shibata K. Yoshino M., Itoh M., Ishii Y., RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., RA Arakawa T., Hara A., Fukunishi Y., Konno H., Nadachi J., Fukuda S., RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., RA Salto T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Salto R., RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., RA Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., RA Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Ra Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Ra Schriml L.M., Stabbli F., Suzuki R., Tomita M., Wagner L., Washio T., RA Schriml L.M., Stabbli F., Suzuki R., Tomita M., Wagner L., Washio T., RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., RA Hyons P., Marchionni L., Mashima J., Mazzarelli J., Wombaerts P., RA Mordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., RA Suzuki H., Toyo-oka K., Wang K.H., Weltz C., Whittaker C., Wilming L., RA Hayashizaki Y., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Pinch C., 
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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PRODOM; PD000657; Adenylate_kin; 1.

PROSITE; PS00113; ADENYLATE_KINASE; 1.

Kinase; Transferase.

NON_TER 232 232

SEQUENCE 232 AA; 25441 MW; 1B74EFD7C97891F2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                         Voncken F., Boxma B., Verhagen E., van Wesel R., van der Drift C., Veenhuis M., Hackstein J., Vogels G.;
"Evidence for a chimeric origin of chytrid hydrogenosomes.";
Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
1- SIMILARITY: BELONGS TO THE ADENYLATE KINASE FAMILY.
EMBL; AJ224659; CAA12056.1; -.
EMBL; AJ224659; CAA12056.1; -.
HSSP; P07170; LAKY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Neocallimastix frontalis (Rumen fungus).
Eukaryota; Fungi; Chytridiomycota; Neocallimasticales;
Neocallimasticaceae; Neocallimastix.
NCBI_TaxID-4757;
[1]
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Pfam; PF00406; adenylatekinase; 1.
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122 LTVDDSLLFKRITGRLVHPASGRSYHKIFNPNQKVEGKDDITGEPLIQRSDDTEAALKKR 181
                                                                                     114 LNVPFEVIKORLTARWIHPASGRVYNIEFNP-PKTVGIDDLTGEPLIQREDDKPETVIKR 172
                                                                                                               Length 232;
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Search completed: March 19, 2003, 16:32:44 Job time : 1423 secs

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Listing first 45 summaries
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B29792
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S44766
JQ1944
AC0563
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H97282
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J01945
KIHU945
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S23568
T44404
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214 2217 2062 2199 2114 2114 2115 2117 2217 2217 2217 2217 2217 2217
0 0 0 0 0 0 H 0 0 0 0 0 0 0 0 0 0 0 0 0
AG0378 DG9334 T259336 G70307 G70307 S70734 B95027 B97898 B97898 S50007 G712547 F71052 E75698

## ALIGNMENTS

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R;Tomasselli, A.G.; Frank, R.; Schiltz, E.

PFEBS Lett. 202, 303-308, 1986

A;Title: The complete primary structure of GTP:AMP phosphotransferase from beef heart
A;Reference number: A24201; MUID:86248102; PMID:3013690

A;Accession: A24201
                                                                                                                                                                                                                                                                                                           A:Introns: 51/1; 91/1; 148/3; 188/2 C;Superfamily: adenylate kinase C;Superfamily: adenylate kinase C;Keywords: ATP; mitochondrion; nucleotide binding; P-loop; phosphotransferase F;2-227/Product: GTP-AMP phosphotransferase, mitochondrial #status predicted <a href="fitted-color: binding motif A">fitted-color: binding motif A</a> (P-loop)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nucleoside-triphosphate-adenylate kinase (EC 2.7.4.10) 3, mitochondrial - bovine N;Alternate names: adenylate kinase 3 C;Species: Bos primigenius taurus (cattle) C;Date: 15-Jun-1990 #sequence_revision 15-Jun-1990 #text_change 03-Jun-2002 C;Accession: A34442; JH0512; A24201 R;Yamada, M.; Shahjahan, M.; Tanabe, T.; Kishi, F.; Nakazawa, A. Biol. Chem. 264, 19192-19199, 1989
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-50 <SHA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Status: translation not shown
                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                         121
                                                                                                                                              IKQRLTARWIHPASGRYYNIEFNPPKTYGIDDLTGEPLIQREDDKPETYIKRLKAYEDQT
                                                                                        DQGKLIPDDVMTRLALHELKNLTQYSWLLDGFPRTLPQAEALDRAYQIDTVINLNVPFEV 120
                                                                  DQGKLIPDDVMTRLVLHELKNLTQYNWLLDGFPRTLPQAEALDRAYQIDTVINLNVPFEV
                                                                                                                                                                                                                                  208;
                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                94.0%; Score 1091; DB 2;
91.6%; Pred. No. 5.8e-85;
tive 10; Mismatches 9;
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A;Title: Characterization of human adenylate kinase 3 (AK3) cDNA and mapping of the AK3 A;Reference number: A42820; MUID:92347846; PMID:1639383
A;Reference number: A42820; MUID:92347846; PMID:1639383
A;Reference number: A42820
A;Reference number: A42820
A;Reference number: A42820
A;Rolecule type: mRNA
A;Residues: 1-223 <XUG>
A;Cross-references: EMBL:X60673; NID:928576; PIDN:CAA43088.1; PID:928577; GB:S41502
A;Cross-references: EMBL:X60673; NID:928576; PIDN:CAA43088.1; PID:928577; GB:S41502
A;Cross-references: Grontal-cortex
A;Note: sequence extracted from NCBI backbone (NCBIN:109644, NCBIP:109645)
C;Comment: This isozyme is found in the mitochondrial matrix.
C;Genetics:
A;Gene: GDB:AK3
A;Cross-references: GDB:118988; OMIM:103030
A;Map position: 9pter-9p13
A;Cross-references: GDB:118988; OMIM:103030
A;Map position: catalyzes the reversible phosphorylation of adenine monophosphate with nu A;Note: GTP is preferred to ATP as a substrate
C;Superfamily: adenylate kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                            ucleoside-triphosphate-adenylate kinase (EC 2.7.4.10) 3 - human ;Alternate names: adenylate kinase 3 C;Species: Homo sapiens (man) C;Date: 17-Apr-1993 #sequence_revision 23-Mar-1995 #text_change 03-Jun-2002 C;Accession: A42820; S16380; S16381 R;XU, G; O'Connell, P; Stevens, J.; White, R. Genomics 13, 537-542, 1992
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C;Keywords: ATP; GTP; mitochondrior
F;14-21/Region: nucleotide-binding
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C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_
C;Accession: JO1945
R;Tanabe, T.; Yamada, M.; Noma, T.; Kajii, T.; Nakazawa,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
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A;Title: Tissue-specific and developmentally regulated A;Reference number: PQ0534; MUID:93224500; PMID:8468325
A;Accession: JQ1945
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A; Residues: 1-227 <TAN>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KXVLXYYQKKGVLETFSGTETNKIWPYVYAFLQTKVPQRSQKASVTP 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IKQRLTARWIHPASGRVYNIEFNPPKTVGIDDLTGEPLIQREDDKPETVIKRLKAYEDQT
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90.3%;
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Pred. No. 1.8e
6; Mismatches
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1.8e-80;
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                                                                                                                                                                                                                                C;Keywords: ATP; monomer; P-loop; phosphotransferase F;7-14/Region: nucleotide-binding motif A (P-loop) # F;80-85/Region: nucleotide-binding motif B #status a
                                                                                                                                                                                                                                                                                      A; Note: magnesium required C; Superfamily: adenylate kinase C; Keywords: ATP; monomer; P-loop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-77, 'A', 79-214 <MAS>
A; Cross-references: EMBL:X57315;
                                                                                                                                                                                                                                                                                                                                                                                      A;Gene: adk
C;Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Experimental source: strain C; Genetics:
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Matches Best Query Match

Similarity

38.5%;

Score 447.5; Pred. No. 1.5

Conservative

37;

Mismatches

nes 61; DΒ 2

Indels Length

13;

Gaps

4

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RM7004

NID:g43587; PIDN:CAA40570.1; PID:g4359;

LRAVIMGAPGSGKGTVSSRITTHFELKHLSSGDLLRDNMLRGTEIGVLAKAFIDQGKLIP MKIILLGAPGAGKGTQAQFIMNKFGIPQISTGDMFRAAIKAGTELGKQAKALMDEGKLVP

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A;Cross-references: GB:U32719; GB:L42023; NID:g1573310; PIDN:AAC22010.1; PII A;Experimental source: strain Rd KW20 R;Maskell, D.J.; Szabo, M.J.; Butler, P.D.; Williams, A.E.; Moxon, E.R. Moll. Microbiol. 5, 1013-1022, 1991
A;Title: Molecular analysis of a complex locus from Haemophilus influenzae A;Reference number: S15287; MUID:92065797; PMID:1956282
                                                                                                                                                                                                                                                           A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, A;Title: Whole-genome random sequencing and assembly of Haemophilus influe A;Reference number: A64000; MUID:95350630; PMID:7542800 A;Recession: I64062 A;Status: nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                            C;Accession: I64062; S15290
R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M. Science 269, 496-512, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 18-Jun-1999
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A; Accession: S15290
                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-214 <TIGR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           adenylate kinase (EC 2.7.4.3) - Haemophilus influenzae (strain Rd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Species: Haemophilus influenzae
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      184 LXYYQKKGVLETFSGTETNKIWPYVYAFLQTKV-PQRSQKA 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            124 RLTARWIHPASGRVYNIEFNPPKTVGIDDLTGEPLIQREDDKPETVIKRLKAYEDQTKXV 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62 LLVPDHVITRLMMSELENRRGQHWLLDGFPRTLGQAEALDKICEVDLVISLNIPFETLKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 SARLLRAVIMGAPGSGKGTVSSRITTHFELKHLSSGDLLRDNMLRGTEIGVLAKAFIDQG
:::||||||:|: ||:|: ||:|:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KLIPDDVMTRLALHELKNLTQYSWLLDGFPRTLPQAEALDRAYQIDTVINLNVPFEVIKQ 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RLSRRWIHPPSGRVYNLDFNPPHVHGIDDVTGEPLVQQEDDKPEAVAARLRQYKDVAKPV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              130;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60.3%;
58.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 700.5; DB 1; Pred. No. 6.2e-52;
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adenylate kinase (EC 2.7.4.3) ADK2 - yeast (Saccharomyces cerevisiae)
N.Alternate names: PAK3 protein; protein YER170w
C; Species: Saccharomyces cerevisiae
:;Date: 12-Mar-1993 #sequence_revision
C;Accession: S23568; JC1135; S50673
R;Schricker, R.; Magdolen, V.; Bandlow, W.
Mol. Gen. Genet. 233, 363-371, 1992
A;Title: A new member of the adenylate kinase family in yeast: PAK3 is high A;Accession: S23568; MUID:92318888; PMID:1620094
A;Accession: S23568
                                                                                                                                                                                                                                                                                                                                                             A;Description: phosphotransferase
C;Superfamily: adenylate kinase
C;Keywords: ATP; mitochondrion; nucleotide binding;
F;21-28/Region: nucleotide-binding motif A (P-loop)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R:Cooper, A.J.; Friedberg, E.C. Gene 114, 145-148, 1992
A:Title: A putative second adenylate kinase-encoding gene A;Reference number: JC1135; MUID:92267376; PMID:1587477
A;Accession: JC1135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      submitted to the EMBL Data Library, December 1994 A; Description: The sequence of S. cerevisiae cosmids 9163 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-225 <SCH>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       \;Gene: SGD:ADK2; PAK3
A;Cross-references: SG
A;Map position: 5R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Dietrich,
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A; Residues: 1-225 <COO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-225 <DIE>
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A; Accession: S50673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GB:M77757; NID:g171045; PIDN:AAA34418.1; PID:g171046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;Cross-references: EMBL:U18922; NID:g603405;
                                                                                                                                                                                                                                                                                                               Query Match
Best Local
                                                                                                                                                                                                                                                                                        Matches
      178
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                                                                                                                                                                  67
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                                                                                                                                                                                                                                             8 LRAVIMGAPGSGKGTVSSRITTHF-ELKHLSSGDLLRDNMLRGTEIGVLAKAFIDQGKLI 66
    DQTKXVLXYYQKKGVLETFSGTETNKI 204
                                                                  FEVIKQRLTARWIHPASGRVYNIEFNPPKTVGIDDLTGEPLIQREDDKPETVIKRLKAYE 177
                                                                                                                                               PDDVMTRLALHELKNL----TQYSWLLDGFPRTLPQAEALDRAYQ-----IDTVINLNVP 117
                                                                                                                                                                                                     LRLLLLGAPGSGKGTQTSRLLKQIPQLSSISSGDILRQEIKSESTLGREATTYIAQGKLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PLIDYYQAEAKAGNTQYFRLDGTQKV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DD-----VMTRLALHELKNLTQYSWLLDGFPRTLPQAEAL-DRAYQIDTVINLNVPFEVI
                                           ESTILERIENRYVHVPSGRVYNLQYNPPKVPGLDDITGEPLTKRLDDTAEVFKKRLEEYK 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DELTVALVKDRIAQADCTN----GFLLDGFPRTIPQADALKDSGVKIDFVLEFDVPDEVI 116
                                                                                                                        PDDLITRLITERLSALGWLKPSAMWLLDGFPRTTAQASALDELLKQHDASLNLVVELDVP 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               F.S.
                                                                                                                                                                                                                                                                                        93; Conser
                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                       37.98;
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                                                                                                                                                                                                                                                                                                         Score 439.5; DB:
Pred. No. 7.6e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MIPS:YER170w
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIDN:AAB64697.1; PID:g603411; MIPS:YER170w
                                                                                                                                                                                                                                                                                                                          DB 2;
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                                                                                                                                                                                                                                                                                    11;
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                                                                                                                                                                                                                                                                                                       RESULT 7
S31338
A;Cross-references: EMBL:X70363;
A;Note: sequence extracted from I
                                                          A; Molecule type: DNA
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C;Keywords: phosphotransferase
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                                         A; Residues: 1-220 < KO2>
                                                                                 A;Status: preliminary
                                                                                                                                                                                R; Konrad,
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A; Residues: 1-217 <STO>
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Best Local
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KTNEPLKDYYKKSGIFGTVSG-ETSDI
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C;Date: 31-Jan-2000 #sequence_revision 31-Jan-2000 #text_change 15-Jun-2001 C;Accession: T44404; C83669 R;Takami, H.; Takaki, Y.: Nataern
                                                                                                                                                                 J. Biol. Chem. 268, 11326-11334, 1993
A;Title: Molecular analysis of the essential gene for adenylate kinase
A;Reference number: A46718; MUID:93266590; PMID:8496185
A;Accession: A46718
                                                                                                                                                                                                                                                                                                                              C;Species: Schizosaccharomyces pombe
C;Date: 30-Sep-1993 #sequence_revision
C;Accession: A46718; T38862; S31338
                                                                                                                                                                                                                                                                                                                                                                                                                                  adenylate kinase (EC 2.7.4.3) 1 - fission yeast (Schizosaccharomyces N;Alternate names: ATP-AMP transphosphorylase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: GB:AP001507; GB:BA000004; NID:g10172612; PIDN:BAB03874.1; GSPDB:GA;Experimental source: strain C-125
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A; Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans A; Reference number: A83650; MUID:20512582; PMID:11058132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: EMBL:AB017508; NID:g4512395; PIDN:BAA75292.1; A;Experimental source: strain C-125
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A;Title: Sequence analysis of a 32-kb region including the major ribosomal protein A;Reference number: 222756; MUID:99209008; PMID:10192928
A;Accession: T44404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KORLTARWIHPASGRVYNIEFNPPKTVGIDDLTGEPLIQREDDKPETVIKRLKAYEDOTK 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MNLILMGLPGAGKGTQAEKIIEKYGIPHISTGDMFRAAMKNETELGLKAKSYMDAGELVP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MDRLTGRRVSPTSGRTYHVIFNPPKVEGICDVDGSELIQRDDDKPETVKKRLEVNQKQAQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DEVTIGIVRDRLSQDDCQNGFLLDGFPRTVAQAEALEDILASLDKKLDYVINIDVPEQLL 120
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42.7%;
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NID: g5535; PIDN: CAA49826.1; NCBI backbone (NCBIN: 132838,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 437; DB
Pred. No. 1.2e
47; Mismatches
                                                                                                                                                                                                                                                                                                                                                                    30-Sep-1993 #text_change 10-Dec-1999
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   PID:g5536
NCBIP:132839)
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A; Map position: 1
C: Function:
A; Description: catalyzes reversib
A; Note: magnesium required
C; Superfamily: adenylate kinase
C; Superfamily: adenylate kinase
C; Keywords: ATP; P-loop; phosphot
F; 10-17/Region: nucleotide-bindin
F; 84-89/Region: nucleotide-bindin
F; 31,88,134/Active site: His, Asp
                                                                                      A:Cross-references: EMBL:M18455; NID:g171030; A:Note: the nucleotide sequence was submitted R;Davies, C.J.: Hutchison III, C.A. Nucleic Acids Res. 23, 507-514, 1995
                                                                                                                                                                                                                                        R; Konrad, M.

J. Biol. Chem. 263, 19468-19474, 1988

A;Title: Analysis and in vivo disruption of the gene coding A; Reference number: A32539; MUID:89066766; PMID:2848829

A; Roccession: A32539

A; Accession: A32539
                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Saccharomyces cerevisiae
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 15-Sep-2000
C;Accession: S05799; A3539; S53987; A25855; A25411; S59433; S47475; S47934;
;Magdolen, V: Gechsner, U: Bandlow, W.
urr. Genet. 12, 405-411, 1987
A;Title: The complete nucleotide sequence of the gene coding for yeast adenyl A;Reference number: S05799; MUID:88194690; PMID:2834097
A;Accession: S05799
                       A; Reference number: S53985; A; Accession: S53987
                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-222 <KON>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      adenylate kinase (EC 2.7.4.3) [validated] - yeast (Saccharomyces cerevisiae) N;Alternate names: ATP-AMP transphosphorylase; protein YD9934.11; protein YDC;Species: Saccharomyces cerevisiae
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                                                                                                                                                                                                                                   A; Status: nucleic acid sequence
                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-222 <MAG>
A; Cross references: EMB
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submitted to the EMBL Data Li
A;Reference number: Z21732
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Best Local
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                                             Insertion site specificity of the transposon Tn3 nce number: S53985; MUID:95192063; PMID:7885847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TPVVEFYKKKGKWAAVDAAQKPEQVWEQIVAILE
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acid sequence
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Library, February 1996
                                                                                                                                                                                                                                 not shown;
  not shown;
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translation
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                                                                                                                                      PIDN:AAA66319.1;
to the EMBL Data
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                                                                                                                                      Library, July 1988
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A;Description: catalyzes the reversible phosphorylation or adenine mu C;Superfamily: adenylate kinase C;Keywords: acetylated amino end; ATP; P-loop; phosphotransferase F;3-222/Product: adenylate kinase #status experimental <MAT> F;3-222/Product: adenylate kinase #status experimental <MAT> F;3-20/Region: nucleotide-binding motif A (P-loop) #status atypical F;87-92/Region: nucleotide-binding motif B #status atypical F;3/Modified site: acetylated amino end (Ser) (in mature form) #status F;34,91/Active site: His, Asp #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Experimental source: strain AB972
R; Abele, U.; Schulz, G.E.
submitted to the Brookhaven Protein Data Bank, July
A; Reference number: A65089; PDB: IAKY
A; Contents: annotation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross references: EMBL:Y00413; NID:g3340; PIDN:CAA68471.1; PA;Note: the authors translated the codon GAA for residues 115; R;Tomassell1, A.G.; Mast, E.; Janes, W.; Schiltz, E. Eur. J. Biochem. 155, 111-119, 1986
A:Title: The complete amino acid sequence of adenylate kinase A;Reference number: A25411; MUID:86136113; PMID:3004985
A;Accession: A25411
A;Residues: 3-221,'N' <TOM>
R;Murphy, L.; Harris, D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Title: High-resolution structures of adenylate kinase from A; Reference number: A56505; MUID:95400193; PMID:7670369 A; Contents: annotation; X-ray crystallography, 1.63 angstroms
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C; Function:
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A;Cross-references: SGD:S0002634; MI
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A; Residues: 1-222 < MUR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Genetics:
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Protein Sci. 4, 1262-1271, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Contents: annotation; X-ray crystallography, 1.63 angstroms,
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A; Residues: 1-138, 'R', 140-222 < PRO>
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Nucleic Acids Res. 15, 7187, 1987
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A; Residues: 1-222 <DAV>
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Best Local
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182
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                                   YEDQTKXVLXYYQKKGVLETFSGTETNKIWPYVYAFLQTKV 216
                                                                                                                                                                                                                                            GGLVSDDIMVNMIKDELTNNPACKNGFILDGFPRTIPQAEKLDQMLKEQGTPLEKAIELK 121
                                                                                                                                                                                                                                                                                           GKLIPDDVMTRLALHELKN--LTQYSWLLDGFPRTLPQAEALDRAYQ-----IDTVINLN 115
                                                                                                                  VDDELLVARITGRLIHPASGRSYHKIFNPPKEDMKDDVTGEALVQRSDDNADALKKRLAA
                                                                                                                                                                            VPFEVIKORLTARWIHPASGRVYNIEFNPPKTVGIDDLTGEPLIOREDDKPETVIKRLKA 175
                                                                                                                                                                                                                                                                                                                                                                  SSSESIRMVLIGPPGAGKGTQAPNLQERFHAAHLATGDMLRSQIAKGTQLGLEAKKIMDQ
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40.3%;
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115 and 153
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N;Alternate kinase (EC 2.7.4.3) 2 - human
N;Alternate names: ATP-AMP transphosphorylase
C;Species: Homo sapiens (man)
C;Date: 1.Dec:1996 #sequence_revision 06-Jun-1997 #text_change 18-Jun-1999
C;Accession: G02248
R;Choe, I.
        A; Note:
C; Superf
C; Keywor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Note: magnesium required
C; Superfamily: adenylate klnase
C; Keywords: alternative splicing; ATP; P-loop; phosphotransferase
E; 22-29/Region: nucleotide-binding motif A (P-loop) #status atypic
E; 95-100/Region: nucleotide-binding motif B #status atypical
E; 42-92/Disulfide bonds: #status predicted
E; 43,99,145/Active site: His, Asp, His #status predicted
                                                                                                                                                                                                                                                     submitted to the EMBL Data A; Reference number: H00907 A; Accession: G02248
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C;Species: Homo sapiens (man)
C;Date: 18-Mar-1998 #sequence_revision 18-Mar-1998 #text_change 18-Jun-1999
C;Accession: JC5893
                                                               A; Description: catalyzes reversible phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Title: Cloning and expression of human adenylate kinase 2 isozymes: Differential expre
A;Reference number: JC5893; MUID:98162934; PMID:9504408
A;Accession: JC5893
                                                                                                              A;Gene: adk2
                                                                                                                                                     A; Experimental source:
                                                                                                                                                                      A;Cross-references: EMBL:U39945; NID:g1209686;
                                                                                                                                                                                       A; Residues: 1-239 <CHO>
                                                                                                                                                                                                              A; Molecule type: mRNA
                                                                                                                                                                                                                               A; Status: preliminary; translated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           adenylate kinase (EC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Description:
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A;Experlmental source: tissue fetal liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 1-232 <LEE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Function:
                           Superfamily: adenylate kinase
                                                                                           ;Function:
                                                                                                                               Genetics:
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           196 PLIEYYRKRGIHSAIDASQT 215
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                                            magnesium required
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KQRLTARWIHPASGRVYNIEFNPPKTVGIDDLTGEPLIQREDDKPETVIKRLKAYEDQTK 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DEMVVELIEKNLETPLCKNGFLLDGFPRTVRQAEMLDDLMEKRKEKLDSVIEFSIPDSLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IRAVLLGPPGAGKGTQAPRLAENFCVCHLATGDMLRAMVASGSELGKKLKATMDAGKLVS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DDVMTRLALHELKN-LTQYSWLLDGFPRTLPQAEALD-----RAYQIDTVINLNVPFEVI 121
      alternative splicing;
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ATP-AMP transphosphorylase
                                                                                                                                                     tissue
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                                                                                                                                                     fetal liver
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       45;
      ATP;
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Pred. No. 4.2e-29;
                                                                                                                                                                                                                                  from
                                                                                                                                                                                                                                                                                               November 1995
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      P-loop;
                                                                                                                                                                                                                                  GB/EMBL/DDBJ
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      phosphotransferase
                                                                                                                                                                        PIDN: AAC52061.1;
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                                                                    of
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                                                                    ATP
                                                                                                                                                                    PID: g1209687
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A;Note: magnesium required
C;Superfamily: adenylate kinase
C;Superfamily: adenylate kinase
C;Keywords: ATP; P-loop; phosphotransferase
F;7-14/Region: nucleotide-binding motif A (P-loop) #status atypical
F;80-85/Region: nucleotide-binding motif B #status atypical
F;30,84,126/Active site: Ser, Asp, His #status predicted
                                                                                                                               A; Description: catalyzes
                                                                                                                                                 C; Function
                                                                                                                                                                        A;Gene:
                                                                                                                                                                                                            A; Experimental source:
                                                                                                                                                                                                                                  A; Cross-references:
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Genetics:

adk;

NMA1032

reversible phosphorylation

of

AMP

with

ATP ូ

form C WO

ADP

GB:AL162754; ce: serogroup

GB:AL157959; NID:g7379424; A, strain 22491

PIDN:CAB84301.1;

PID:9737

3

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RESULT 11
S61841
                                                                                                                                                    A;Cross-references: EMBL:L36470; NID:g845613; PIDN:AAA99173.1; PID:g845614
A;Experimental source: ATCC 43831
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quall, M.A.; Nature 404, 502-506, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R:Vazquez, J.A.; PELLOW, 1995
MOL. Microbiol. 15, 1001-1007, 1995
A;Title: Interspecies recombination in nature: a meningococcus
A;Title: Interspecies recombination in nature: A meningococcus
A;Title: Interspecies recombination in nature: A meningococcus
                                                                              A;Title: Complete DNA sequence of a serogroup A strain of A;Reference number: A81775; MUID:20222556; PMID:10761919 A;Accession: F81951
                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: EMBL:L36469; NID:g845611; PIDN:AAA99172.1; PID:g845612
A;Experimental source: strain P63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Species: Neisseria meningitidis
A; Variety: strain P63; ATCC 43831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             adenylate kinase (EC 2.7.4.3) [similarity] - Neisseria meningitidis (strain z2491 N, Alternate names: ATP-AMP transphosphorylase
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A; Molecule type: DNA
A; Residues: 1-215 <PAR>
                                                     A;Status:
                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-215 <VAQ>
                                                                                                                                                                                                                                                                                                                                                                        A;Status: nucleic
                                                                                                                                                                                                                                                                                                                                                                                              A; Accession: S61842
                                                                                                                                                                                                                                                                                                                                                                                                                      A; Note: the nucleotide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Date:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: nucleic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27-Apr-1996 #sequence_revision 13-Mar-1997 #text_change 02-Feb-2001
sion: S61841; S61842; F81951
zz, J.A.; Berron, S.; O'Rourke, M.; Carpenter, G.; Feil, E.; Smith,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8 LRAVIMGAPGSGKGTVSSRITTHFELKHLSSGDLLRDNMLRGTEIGVLAKAFIDQGKLIP 67
                                                        preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            XVLXYYQKKGVLETFSGTET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IRRITGRLIHPKSGRSYHEEFNPPKEPMKDDITGEPLIRRSDDNEKALKIRLQAYHTQTT 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DEMVVELIEKNLETPLCKNGFLLDGFPRTVRQAEMLDDLMEKRKEKLDSVIEFSIPDSLL 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IRAVLLGPPGAGKGTQAPRLAENFCVCHLATGDMLRAMVASGSELGKKLKATMDAGKLVS 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PLIEYYRKRGIHSAIDASQT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DDVMTRLALHELKN-LTQYSWLLDGFPRTLPQAEALD-----RAYQIDTVINLNVPFEVI 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             . Similarity
87; Conserv
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                                                                                                                                                                                                                                                                                                                                                                acid sequence not shown;
                                                                                                                                                                                                                                                                                                                                                                                                                      sequence
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Pred. No. 4.3e-
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                                                                                                                                 Neisseria menigitidis 22491
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C;Species: Nelsseria meningitidis
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
C;Accession: F81154
R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B. T.; H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M. Science 287, 1809-1815, 2000
Science 287, 1809-1815, 2000
A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A;Reference number: A81000; MUID:20175755; PMID:10710307
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A;Gene:
C;Superf
RESULT 13
$43016
square kinase (EC 2.7.4.3) - Bordetella pertussis
n;Alternate names; ATP-AMP transphosphorylase
C;Species: Bordetella pertussis
C;Date: 07-Sep-1994 #sequence_revision 10-Nov-1995 #text_change 18-Jun-1999
C;Accession: $43016
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A; Residues: 1-215 <TET>
A; Cross-references: GB: AE002435;
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A; Status: preliminary
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Best Local Similarity
Matches 86; Conserv
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45.7%;
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45.7%;
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Pred. No. 4.6e-29;
Pred. No. 4.6e-29;
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Pred. No. 4.6e-29;
0; Mismatches 52;
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C:Superfamily: adenylate kinase C;Keywords: ATP; P-loop; phosphotransferase C;Keywords: ATP; P-loop; phosphotransferase F;7-14/Region: nucleotide-binding motif A (P-loop) #status atypical F;80-85/Region: nucleotide-binding motif B #status atypical F;30,84,126/Active site: Ser, Asp, His #status predicted
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A;Variety: strain CH-95
C;Date: 27-Apr-1996 #sequence_re
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A;Title: Interspecies recombination in nature: a meningococcus A;Reference number: S61840; MUID:95349386; PMID:7623657
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F;7-14/Region: nucleotide-binding motif A (P-loop) #status atypical
F;80-85/Region: nucleotide-binding motif B #status atypical
F;30,84,126/Active site: Ser, Asp, His #status predicted
                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-215 < VAZ>
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A; Status: nucleic a
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A; Residues: 1-218 <GIL>
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Best Local
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                                   LRAVIMGAPGSGKGTVSSRITTHFELKHLSSGDLLRDNMLRGTEIGVLAKAFIDQGKLIP 67
MKALLLGAPGAGKGTQAQFITAAFGIPQISTGDMLRAAIKAGTPLGLEAKKIIDEGGLVR
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                                                                                                              36.68;
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42.1%;
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Pred. No. 1.2e-28;
0; Mismatches 52;
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Pred. No. 6.9e-29;
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RESULT 15
G83184
adenylate kinase PA3686 [imported] - Pseudomonas aeruginosa (strain PAO1)
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: G83184
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
J. Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathc
A; Reference number: A82950; MUID:20437337; PMID:10984043
A; Accession: G83184
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-215 <STOO
A; Cross-references: GB:AE004788; GB:AE004091; NID:9949846; PIDN:AAG07074.1; GSPDB:GN001
C; Gene: adk; PA3686
C; Superfamily: adenylate kinase
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Search completed: March 19, 2003, 16:44:32 Job time: 694 secs
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Title:
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Listing first 45 summaries
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Maximum DB seq length: 2000000000
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   1086
1046
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   SwissProt_40:*
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X-RAY CRYSTALLOGRAPHY (1.85 ANGSTROMS).

X-RAY CRYSTALLOGRAPHY (1.85 ANGSTROMS).

Diederichs K., Schulz G.E.;

Diederichs K., Schulz G.E.;

"The refined structure of the complex between adenylate kinase from beef heart mitochondrial matrix and its substrate AMP at 1.85-A resolution.";

J. Mol. Biol. 217:541-549(1991).

-I- CATALYTIC ACTIVITY: GTP + AMP = GDP + ADP.

-I- SUBURIT: MONOMER.

-I- SUBURITARITY: BELONGS TO THE ADENYLATE KINASE FAMILY.
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TISSUE-Heart;
TISSUE-86248102; PubMed-3013690;
MEDLINE-86248102; Frank R., Schiltz
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"Cloning and characterization of cDNa
phosphotransferase of bovine liver.",
J. Biol. Chem. 264:19192-19199(1989).
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MEDLINE-90037053; PubMed-2478555;
Yamada M., Shahjahan M., Tanabe T
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MEDLINE-91084487; PubMed-2175649;
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NCBI_TaxID=9913;
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01-NOV-1997
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                                                                                                                                                      SWISS-PROT entry is copyright. It is produced through a ceen the Swiss Institute of Bioinformatics and the EMBL
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1990 (Rel. 14, Last sequence update)
1997 (Rel. 35, Last annotation update)
phosphotransferase mitochondrial (EC
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202:303-308(1986).
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NA for mitochondrial GTP:AMP
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Pfam; PF00406; adenylatekinase; 1.
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PVLEYYRKKGVLETFSGTETNKIWPHVYAFLQTKLPQRSQETSVTP
                        XVLXYYQKKGVLETFSGTETNKIWPYVYAFLQTKVPQRSQKASVTP
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SE; GTP-binding; Mitochondrion; 31

0 GTP (BY SIMILARITY).

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          KAD3_RAT
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O1-APR-1993
O1-NOV-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
-! CATALYTC ACTIVITY: GTP + AMP = GDP + ADP.
-! SUBUNIT: MONOMER (BY SIMILARITY).
-! SUBCELLULAR LOCATION: Mitochondrial matrix (By similarity).
-! SIMILARITY: BELONGS TO THE ADENYLATE KINASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
GTP:AMP phosphotransferase mitochondrial (EC
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30-MAY-2000
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                                                                                                                                                            WIHPASGRVYNIEFNPPKTVGIDDLTGEPLIQREDDKPETVIKRLKAYEDQTKXVLXYYQ
                                                                                                          KKGVLETFSGTETNKIWPHVYSFLQTKVPETTQKASVTP
                                                                                                                                                   WIHPASGRVYNIEFNPPKTVGIDDLTGEPLIQREDDKPETVIKRLKAYEAQTEPVLQYYQ
1993 (Rel. 25, Created)
1993 (Rel. 25, Last sequence update)
1995 (Rel. 32, Last annotation update)
phosphotransferase mitochondrial (EC
                                                                                                                                                                                                                                                                                           Similarity
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Pred. No. 4
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Sciurognathi;
                                                      PRT;
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thi; Muridae; Murinae; Mus
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 2.7.4.10) (AK3).
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KAD4_MOUSE
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DT 30-MAY-2000
DT 16-CCT-2001
DE Adenylate k:
Adenylate k:
Adenylate k:
CR AK4
OR AK4
OS Mus musculus
OC Mammalia; Eukaryota; N
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Rattus norvegicus (Rat).
Rukaryota; Metazoa; Chordata;
Eukaryota; Metazoa; Rodentia;
                                                      30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Adenylate kinase isoenzyme 4, mitochondrial (Firansphosphorylase).
AK4 OR AK-4 OR AK3B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Tanabe T., Yamada M., Noma T., Kajii T., Nakazawa A.;
"Tissue-specific and developmentally regulated expression genes encoding adenylate kinase isozymes.";
J. Biochem. 113:200-207(1993).
-i- CATALYTIC ACTIVITY: GTP + AMP = GDP + ADP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR00094; ADENYLTKNASE.
ProDom; PD000657; Adenylate_kin; 1.
PROSITE; PS00113; ADENYLATE_KINASE; 1.
 Mammalia; Eutheria; NCBI_TaxID=10090;
                               Eukaryota; Metazoa;
                                             Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000850; Adenylate_kin Pfam; PF00406; adenylatekinase; 1.
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HSSP; P08760; 2AK3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Transferase; Kinase;
                                                                                                                                                                                                                                              181 PVLQYYQKKGVLETFSGTETNKIRPHVYSFLQMKVPETIQKASVTP
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                                                                                                                                                                                                                                                                                                                                                                                                                            1 GASGRLLRAVIMGAPGSGKGTGSSRITKHFELKHLSSGDLLRQNMLQGTEIAVLAKSFID
                                                                                                                                                                                                                                                                                                                                                                                                                                            2 GASARLLRAVIMGAPGSGKGTVSSRITTHFELKHLSSGDLLRDNMLRGTEIGVLAKAFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity 90.3
04; Conservative
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226 AA;
                                           (Mouse)
                                                                                                                                                                    STANDARD;
               Chordata;
Rodentia;
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25307
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90.3%;
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0 BY SIMILARITY.
21 GTP (BY SIMILARITY)
25307 MW; D57FF37404AA6625
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Pred. No. 5.4e-82;
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               Craniata; Vertebrata;
Sciurognathi; Muridae;
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                 Muridae;
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                               Euteleostomi;
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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[2]
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SEQUENCE
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MGD; MGI:87980; AK4.

InterPro; IPR000850; Adenylate_kin.

Pfam; PF00406; adenylatekinase; 1.

PRINTS; PR00094; ADENYLTKNASE.

PRODOM; PD000657; Adenylate_kin; 1.

PROSITE; PS00113; ADENYLATE_KINASE; 1.
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"Identification of a novel adenylate kinase system cloning of the fourth adenylate kinase.";
Brain Res. Mol. Brain Res. 62:187-195(1998).
                                                                                                                                                                                                                                                                                                                                                                                 Transferase;
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                                                                                                                                                                                                                                                 SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                              LXYYQKKGVLETFSGTETNKIWPYYYAFLQTKV-PQRSQKA
                                                                                                                                                           RLTARWIHPASGRVYNIEFNPPKTVGIDDLTGEPLIQREDDKPETVIKRLKAYEDQTKXV
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                                                                                                                                                                                                       KLIPDDVMTRLALHELKNLTQYSWLLDGFPRTLPQAEALDRAYQIDTVINLNVPFEVIKQ
                                                                                                   IELYKSRGVLHQFSGTETNRIWPYVYTLFSNKITPIQSKEA
                                                                                                                                                RLSRRWIHPSSGRVYNLDFNPPQVQGIDDITGEPLVQQEDDKPEAVAARLRRYKDAAKPV
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190
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  (Rel.
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                                             STANDARD;
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68 V
187 S
190 V
; 25061 MW;
                                                                                                                                                                                                                                                                                                                        e; GTP-binding; Mitochondrion.
20 GTP (BY SIMILARITY).
68 GTP (BY GIMILARITY).
187 S -> N (IN REF. 2).
190 V -> M (IN REF. 2).
25061 MW; 50552294971515EC CRC
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58.8%;
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 sequence up
annotation
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Pred. No. 4.7e-54;
1; Mismatches 49
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DEPTO

01-AUG-1992 01-AUG-1992 15-JUN-2002 01-AUG-1992 (Rel. 01-AUG-1992 (Rel. 15-JUN-2002 (Rel. Adenylate kinase i

transphosphorylase)

isoenzyme 23, 23, 41,

Last annotation update nzyme 4, mitochondrial Last sequence update)

update)

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2.7.4.3)

KAD4\_HUMAN P27144;

STANDARD;

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                                                                                                                                                                                                                                                                                                                                           NP_BIND
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                  Pfam, PF00406; adenylatekinase; 1.
PRINTS; PR00094; ADENYLTKNASE;
PRODOM; PD000657; Adenylate kin; 1.
PROSITE; PS00113; ADENYLATE_KINASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; D87809; BAA77761.1; -. HSSP; P08760; 2AK3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           <del>;</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-Wistar; TISSUE-Forebrain; medLINE-99033072; PubMed-9813319;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                       Transferase; Kinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yoneda T., Sato M., Maeda M., Takagi H.; "Identification of a novel adenylate kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 transphosphorylase)
                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              denylate kinase isoenzyme
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DEVELOPMENTAL STAGE: EXPRESSED IN THE CENTRAL NERVOUS SYSTEM REGION-SPECIFIC MANNER FROM THE MIDDLE STAGE OF EMBRYOGENESIS THE ADULTHOOD IN THE RODENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: BELONGS TO THE ADENYLATE KINASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HIPPOCAMPUS.
                                                                           LXYYQKKGVLETFSGTETNKIWPYVYAFLQTKV-PQRSQKA
                                                                                                                                                                                      KLIPDDVMTRLALHELKNLTQYSWLLDGFPRTLPQAEALDRAYQIDTVINLNVPFEVIKQ 123
                                                           IELYKSRGVLHQFSGTETNRIWPYVYTLFSNKITPIQSKEA
                                                                                                                                            RLTARWIHPASGRVYNIEFNPPKTVGIDDLTGEPLIQREDDKPETVIKRLKAYEDQTKXV
                                                                                                                                                                                                                               ASKLLRAVILGPPGSGKGTVCERIAQNFGLQHLSSGHLLRENLKTNTEVGDVAKQYLEKG
                                                                                                                                                                                                                                                          SARLLRAVIMGAPGSGKGTVSSRITTHFELKHLSSGDLLRDNMLRGTEIGVLAKAFIDQG
                                                                                                                RLSRRWIHPSSGRVYNLDFNPPQVLGVDDITGEPLVQQEDDKPEALAARLRRYKDAAKPV
                                                                                                                                                                        LLVPDHVITRLMMSELETRSAQHWLLDGFPRTLVQAEALDRICDVDLVISLNIPFETLKD
                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                           IPR000850; Adenylate_kin.
                                                                                                                                                                                                                                                                                                                                             223 AA;
                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                             25203 MW;
                                                                                                                                                                                                                                                                                                  61.0%;
57.9%;
                                                                                                                                                                                                                                                                                                                                          GTP-binding; Mitochondrion.
20 GTP (BY SIMILARITY)
25203 MW; B5A9BE45CFA3C19B
                                                                                                                                                                                                                                                                                    44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4,
                                                                                                                                                                                                                                                                                    Score 708.5; DB 1
Pred. No. 4.7e-54;
4; Mismatches 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mitochondrial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; I
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                               DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (EC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          system
                                                                                       223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Potential).
[DAL CELLS.IN
                                                                                                                                                                                                                                                                                                                                              CRC64;
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                                                                                                                                                                                                                                                                                                                 Length
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; Murinae; Rat
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Best Local S
Matches 13(
              KAD_HAEIN P24323;
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PIR; S16381; S16381.
PIR; S16380; S16380.
PIR; A42820; A42820.
HSSP; P08760; 2AK3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=92347846; PubMed=1639383; Xu G., O'Connell P., Stevens J., White R.; "Characterization of human adenylate kinase 3 of the AK3 pseudogene to an intron of the NF1 Genomics 13:537-542(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                          Transferase; Kinase; NP_BIND 12 SEQUENCE 223 AA;
                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000850; Adenylate_kin.
Pfam; PF00406; adenylatekinase; 1.
PRINTS; PR00094; ADENYLTKNASE.
PRODOm; PD000657; Adenylate_kin; 1.
PROSITE; PS00113; ADENYLATE_KINASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (OCT-2001) to the -!- CATALYTIC ACTIVITY: GTP -!- SUBUNIT: MONOMER.
 01-MAR-1992 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; X60673; CAA43088.1; -. EMBL; BC016180; AAH16180.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SUBCELLULAR LOCATION: Mitochondrial matrix.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-Lung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                              мім; 103030;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genew;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM
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                                                                                                     LXYYQKKGVLETFSGTETNKIWPYVYAFLQTKV-PQRSQKA 223
                                                                                                                                    KLIPDDVMTRLALHELKNLTQYSWLLDGFPRTLPQAEALDRAYQIDTVINLNVPFEVIKQ 123
                                                                                                                                                                                                                                      SARLLRAVIMGAPGSGKGTVSSRITTHFELKHLSSGDLLRDNMLRGTEIGVLAKAFIDQG
                                                                                       IELYKSRGVLHQFSGTETNKIWPYVYTLFSNKITPIQSKEA
                                                                                                                                                                                                                                                                                          al Similarity
130; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                        HGNC:363; AK3.
                                                                                                                                                                                                                                                                                          Conservative
                          STANDARD;
 Created)
                                                                                                                                                                                                                                                                                                                             20
25268 MW;
                                                                                                                                                                                                                                                                                                    58.8%;
                                                                                                                                                                                                                                                                                                                                       GTP-binding; Mitochondrion.
20 GTP (BY SIMILARITY).
25268 MW; 653341A8EB3BC723 CRC64;
                                                                                                                                                                                                                                                                                          38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL/GenBank/DDBJ
+ AMP = GDP + ADP.
                                                                                                                                                                                                                                                                                       Score 700.5;
Pred. No. 2.3e
8; Mismatches
                        B
                                                                                                                                                                                                                                                                                                     3e-53;
                                                                                                                                                                                                                                                                                                                DB 1;
                                                                                                                                                                                                                                                                                       52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (AK3) cDNA and gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               databases
                                                                                                                                                                                                                                                                                                               Length 223;
                                                                                                                                                                                                                                                                                          Indels
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                                                                                                                                                                                                                                                                                        1.
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LRAVIMGAPGSGKGTVSSRITTHFELKHLSSGDLLRDNMLRGTEIGVLAKAFIDQGKLIP

60

MKIILLGAPGAGKGTQAQFIMNKFGIPQISTGDMFRAAIKAGTELGKQAKALMDEGKLVP

-VMTRLALHELKNLTQYSWLLDGFPRTLPQAEAL-DRAYQIDTVINLNVPFEVI 121

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Best Loc
Matches
                                   Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-92065797; PubMed-1956282; Maskell D.J., Szabo M.J. Putter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1995 (Rel. 32, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Adenylate kinase (EC 2.7.4.3) (ATP-AMP transp
                                                                       Transferase; Kinase; ATP-binding; Complete proteome.

NP_BIND
7 15 ATP (BY SIMILARITY).

CONFLICT 78 78 T -> A (IN REF. 1).

SEQUENCE 214 AA; 23508 MW; B83B630EE9E1AACF CRC6
                                                                                                                                                                                                                                                                     EMBL; X57315; CAA40570.1; -. EMBL; U32719; AAC22010.1; -. PIR; S15290; S15290.
                                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.lsb-slb.ch/announce/or send an email to license@isb-slb.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                       This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Science 269:496-512(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAID-Rd / KW20 / ATCC 51907;
MEDLINE-95350630; PubMed-7542800;
MEDLINE-95350630; Adams M D. Whi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               involved in phase-variable lipopolysaccharide Mol. Microbiol. 5:1013-1022(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Haemophilus influenzae.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADK OR HI0349
                                                                                                                                        PRINTS; PR00094; ADENYLTKNASE.
PRODOM; PD000657; Adenylate_kin; 1.
PROSITE; PS00113; ADENYLATE_KINASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                        between
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=727;
                                                                                                                                                                                                                                                    HSSP; P05082; 1E4Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Venter J.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Maskell D.J., Szabo M.J., Butler P.D., Molecular analysis of a complex locus
                                                                                                                                                                                                Pfam; PF00406; adenylatekinase; 1.
                                                                                                                                                                                                                                    rigr; HI0349;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Whole-genome random sequencing and assembly of Haemophilus influenzae
                                                                                                                                                                                                                   nterPro; IPR000850; Adenylate_kin.
                    Local
                                                                                                                                                                                                                                                                                                                                                                                               s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation European Bioinformatics Institute. There are no restrictions on it by non-profit institutions as long as its content is in no we
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBUNIT: MONOMER (BY SIMILARITY).
SUBCELLULAR LOCATION: Cytoplasmic.
SIMILARITY: BELONGS TO THE ADENYLATE KINASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             THE PATHOGENESIS OF H. INFLUENZAE.

CATALYTIC ACTIVITY: ATP + AMP = ADP +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: THIS SMALL UBIQUITOUS ENZYME IS ESSENTIAL FOR MAINTENANCE AND CELL GROWTH. IT MAY BE LINKED TO THE BIOSYNTHESIS OF LIPOPOLYSACCHARIDE SURFACE MOLECULES, WHICH ARE IMPORTANT FOR
                  Similarity
   Conservative
                  38.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gamma subdivision; Pasteurellaceae;
   37;
                  Score 447.5; DB Pred. No. 1.3e-31
                                                                          B83B630EE9E1AACF CRC64;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Williams A.E., Mc
from Haemophilus
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                                       DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADP
   61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ims A.E., Moxon E.R.;
aemophilus influenzae
biosynthesis.";
                                   Length
   Indels
                                       214;
   13;
                                                                                                                                                                                                                                                                                                                                                                                                                                        a collaboration
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S., Arlat M., Billault A., Brottler P., Camus J.C., Cattolico L., Chandler M., Choisane N., Claudel-Renard C., Cunnac S., Demange N., Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schlex T., Siguier P., Thebault P., Whalen M., Wincker P., Levy M., Weissenbach J., Boucher C.A., "Genome sequence of the plant pathogen Ralstonia solanacearum."; Nature 415:497-502(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation updat
Adenylate kinase (EC 2.7.4.3) (ATP-AMP tran
ADK OR RSC2533 OR RS05765.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KAD_RALSO
Q8XWE1;
                                                                                                                                                                                                                                                                                                                                             Transferase; Kinase; ATP-binding; Complete proteome.

NP_BIND 7 15 ATP (BY SIMILARITY).

SEQUENCE 222 AA; 24223 MW; CB3B975CB93734A8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PR00094; ADENYLTKNASE.
PRODOM; PD000657; Adenylate_kin; 1.
PROSITE; PS00113; ADENYLATE_KINASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ralstonia solanacearum (Pseudomonas solanacearum).
Bacteria; Proteobacteria; beta subdivision; Ralstonia group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AL646070; CAD16240.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=21681879; PubMed=11823852;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=305;
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           61
                                                              68
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                                                                                                                                                                               8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBUNIT: Monomer (By similarity).
SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
SIMILARITY: BELONGS TO THE ADENYLATE KINASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                maintenance and cell growth.

CATALYTIC ACTIVITY: ATP + AMP - ADP + ADP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION: This small ubiquitous enzyme is
                             DDVM-----TRLALHELKNLTQYSWLLDGFPRTLPQAEAL-DRAYQIDTVINLNVPFEVI 121
                                                                                                                                                    LRAVIMGAPGSGKGTVSSRITTHFELKHLSSGDLLRDNMLRGTEIGVLAKAFIDQGKLIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DDIIIGLVKDRLQQSDCKN----GYLFDGFPRTIPQAEAMKDAGVPIDYVLEIDVPFDAI
                                                                                                                 MRLILLGAPGAGKGTQAKFICERFGIPQISTGDMLRAAVKAGTPLGIEAKKVMDAGGLVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PF00406; adenylatekinase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    XVLXYYQ---KKGVLETFSGTETNKI
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                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                               38.3%;
                                                                                                                                                                                                                                     41;
                                                                                                                                                                                                                                  Score 445; DB 1;
Pred. No. 2.3e-31;
1; Mismatches 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    204
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  116
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RESULT 10

KAD_PASMU
ID KAD_PASMU
ID FAD, P
AC P5783

PT 16-OC
DT 16-OC
DT 16-OC
DT 16-OC
DT Adeny
GN ADKO
OOS PASte
OC PASTE
OX NCB1_
RN [1]
RN SEDUI
RA MADDII
RA MEDLII
CC OT STAII
CC OT STAII
DR HESSP
DR INTENI
DR HESSP
DR INTENI
DR PROS
KW Trani
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SQ SEQUI
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Best Local :
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P57837;
16-OCT-2001
16-OCT-2001
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR000850; Adenylate_kin
Pfam; PF00406; adenylatekinase; 1
PRINTS; PR00094; ADENYLTKNASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                     ProDom; PD000657; Adenylate_kin; 1.
PROSITE; PS00113; ADENYLATE_KINASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AE006063; AAK02368.1; -. HSSP; P05082; 1E4V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-OCT-2001 (Rel. 40,
16-OCT-2001 (Rel. 40,
16-OCT-2001 (Rel. 40,
Adenylate kinase (EC 2
                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                           NP_BIND
                                                                                                                                                                                                                                                                                                                        Transferase; Kinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entities requires a license agreement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=21145866; PubMed=11248100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-Pm70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADK OR PM0284.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=747;
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                                 121
                                                                126
 186
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                                                                                               61
                                                                                                                             83
                                                                                                                                                                                          8 LRAVIMGAPGSGKGTVSSRITTHFELKHLSSGDLLRDNMLRGTEIGVLAKAFIDQGKLIP
                                                                                                             DDVMTRLALHELKNL-TQYSWLLDGFPRTLPQAEALDR-AYQIDTVINLNVPFEEVIKQRL 125
                                              TARWIHPASGRVYNIEFNPPKTVGIDDLTGEPLIQREDDKPETVIKRLKAYEDQTKXVLX 185
 YYQ---KKGVLETFSGTETNKI 204
                                 SGRRVHQASGRTYHVVYNPPKVEGKDDVTGEDLIIRADDKPETVLDRLKVYHSTTKPLVD
                                                                                              DDLIISLVKERVAQADCAKGFLLDGFPRTIPQADALKTVGIQIDYVLEFDVPDEVIVERM
                                                                                                                                                           MKIILLGAPGAGKGTQAQFIMNKFGIPQISTGDMLRGAIKAGTDLGKQAKTLMDAGQLVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PLVDYY -- SGWAE -- NGNGAAKVAPPKY 200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KORLTARWIHPASGRVYNIEFNPPKTVGIDDLTGEPLIQREDDKPETVIKRLKAYEDQTK
                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                        214 AA; 23461 MW;
                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                          37.9%;
45.0%;
                                                                                                                                                                                                                                                                                                         ATP-binding; Complete proteome.
15 ATP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , Last sequence update)
, Last annotation update)
2.7.4.3) (ATP-AMP transphosphorylase).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gamma subdivision; Pasteurellaceae
                                                                                                                                                                                                                        38;
                                                                                                                                                                                                                          Pred. No. 5.4
8; Mismatches
                                                                                                                                                                                                                                         Score 440.5; DB 1
Pred. No. 5.4e-31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                        3223D245A3C1432F CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                214
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                B
                                                                                                                                                                                                                                                         DB 1;
                                                                                                                                                                                                                           68;
                                                                                                                                                                                                                                                         Length
                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                         214;
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181

YYQAEAKAGNTKYFRLDGTKKV

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RESULT 11
KADZ_YKADZ_Y
KADZ_Y
KADZ_Y
KADZ_Y
KADZ_Y
KADZ_Y
AC P26364
AC P26366
DT 01-AUG
DT 15-JUL
DT AGE
DT 01-AUG
CO Saccha
RA NCB1_T
RA SCHIL
RA AVILE
CC -1- FU
CC OI Sen
CC -1- FU
CC OI SEN
CC This S
CC OI SEN
CC C STRAIN
RA AVILE
CC OI SEN
CC THIS
RA AVILE
CC OI SEN
CC THIS

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C. STRAIN-228C / AB972;
C. STRAIN-228C / AB972;
C. Dietrich F.S., Mulligan J.T., Hennessey K.M., Allen E., Araujo R.,
A Aviles E., Berno A., Brennan T., Carpenter J., Chen E., Cherry J.M.
A Chung E., Duncan M., Guzman E., Hartzell G., Hunicke-Smith S.,
A Hyman R., Kayser A., Komp C., Lashkari D., Lew H., Lin D.,
A Mosedale D., Nakahara K., Namath A., Norgren R., Oefner P., Oh C.,
A Mosedale D., Nakahara K., Namath A., Norgren R., Shogren T., Smith V.,
A Petel F.X., Roberts D., Sehl P., Schramm S., Shogren T., Smith V.,
A Taylor P., Wei Y., Yelton M., Botstein D., Davis R. W.;
Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
C. TURCTION: THIS SMALL UBIQUITOUS ENZYME IS ESSENTIAL FOR
MAINTENANCE AND CELL GROWTH.
C. MAINTENANCE AND CELL GROWTH.
C. TORTALYTIC ACTIVITY: ATP + AMP = ADP + ADP.
C. I SUBCELLULAR LOCATION: Mitcohondrial.
C. SUBCELLULAR LOCATION: Mitcohondrial.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
Adenylate kinase 2 (EC 2.7.4.3) (ATP-AMP tran.
ADK2 OR PAK3 OR YER170W.
                                                                                       HSSP; P08766; 2AK3.
SGD; S0000972; ADK2.
InterPro; IPR000850; Adenylate_kin.
Pfam; PF00406; adenylatekinase; 1.
PRINTS; PR00094; ADENYLTKNASE.
ProDom; PD000657; Adenylate_kin; 1.
PROSITE; PS00113; ADENYLATE_KINASE; 1.
                                                                                                                                                                                                                                                                                                               EMBL; M77757; AAA34418.1; -.
EMBL; X65126; CAA46254.1; -.
EMBL; U18922; AAB64697.1; -.
PIR; JC1135; JC1135.
PIR; S23568; S23568.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=92318888; PubMed=1620094; Schricker R., Magdolen V., Bandlow W.; "A new member of the adenylate kinase family homologous to mammalian AK3 and is targeted two.l. Gen. Genet. 233:363-371(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KAD2_YEAST
P26364;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cooper A.J., Friedberg E.C.;
"A putative second adenylate kinase-encoding gene from the yeast Saccharomyces cerevisiae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADK2 OR PAK3 OR YER110W.
Saccharomyces cerevisione (Baker's yeast).
Eukaryota; Fung1; Ascomycota; Saccharomyc
Saccharomycetales; Saccharomycetaceae; Sa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDLINE 92267376; PubMed = 1587477;
                                     Transferase; Kinase;
NP_BIND 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: BELONGS TO THE ADENYLATE KINASE FAMILY.
   225
   Ã,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
   25194
                              ATP-binding; Mitochondrion.
29 ATP (BY SIMILARITY)
   WW;
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   3B192BE2535BF91F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  225
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to mitochondria
   CRC64;
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RESULT 12

KAD_ARAH

ID ARADAI

AC 08251

DT 15-JUI

DT 15-JUI

DT 15-JUI

DT ALGEN

GARAN

RA Weers

CC STRAII

RA WEDLI

RA Tabat

RA Tabat

RA Tabat

CC -1-- G

CC -1-
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Best Local
                                                                                                                  EMBL; AF082882;
EMBL; AB007649;
HSSP; P07170; 1A
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STANDARD; PRT; 246 AA.
082514; Q9FWN2;
16-OCT-2001 (Rel. 40, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Adenylate kinase (EC 2.7.4.3) (ATP-AMP transphosphorylase).
ADKI OR AT5G63400 OR MLE2.3.
Arabidopsis thallana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trache Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons II. Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Weers B., Thornburg R.; "Characterization of the adenylate kinase.";
                                                                                                                                                                                                                                                             use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rabata Y., Sato S., Kaneko T., ITabata c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. STRAIN-cv. Columbia;
                                                                                                                                                                                                                or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                           entities
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                                                                                                                                                                                                                                         requires a license agreement (See http://www.isb-sib.ch/announce/
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InterPro; IPR000850; Adenylate\_kin.
Pfam; PF00406; adenylatekinase; 1.
PRINTS; PR00094; ADENYLTKNASE.
ProDom; PD000657; Adenylate\_kin; 1.
PROSITE; PS00113; ADPNYLTAME.

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RESULT 13
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-C-125 / JCM 9153;
MEDLINE-20512582; PubMed-11058132;
Takami H., Nakasone K., Takaki Y.,
Fuji F., Hirama C., Nakamura Y., O
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                                                                                                                                             Kang S.K., Kudo T., Horikoshi K.;

"Molecular cloning and characterization of an alkalophilic
sp. C125 gene homologous to Bacillus subtilis secy.";

J. Gen. Microbiol. 138:1365-1370(1992).
1- FUNCTION: THIS SMALL UBIQUITOUS ENZYME IS ESSENTIAL FOR
MAINTENANCE AND CELL GROWTH.
-I- CATALYTIC ACTIVITY: ATP + AMP = ADP + ADP.
                                                                                                                                                                                                                                                                                                             MEDLINE=92381482; PubMed=1512566;
                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 1-107 FROM N.A. STRAIN-C-125 / JCM 9153;
                                                                                                                                                                                                                                                                                                                                                                                                     "Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and genomic sequence comparison with Bacillus subtilis."; Nucleic Acids Res. 28:4317-4331(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-99209008; PubMed-10192928; Takami H., Takaki Y., Nakasone K., Hirama C., Inoue A., Horikoshi K.; "Sequence analysis of a 32-kb region including the major ribosomal protein gene clusters from alkaliphilic Bacillus sp. strain C-125."; Biosci. Biotechnol. Biochem. 63:452-455(1999).
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STRAIN=C-125 / JC
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Bacteria; Firmicutes;
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SIMILARITY: BELONGS TO
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26932 MW;
       Institute
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45.6%;
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48 ATP (BY SIMILARITY).
52 LINFAIDDAI -> STILLMTQS (II
26932 MW; 659903FBD84B39C7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacillales;
                             copyright.
                                                                    Cytoplasmic.
O THE ADENYLATE KINASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41;
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Pred. No. 1
       Bioinformatics
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ogasawara N.,
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P transphosphorylase).
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.1e-30;
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                          produced through
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               , Sasaki R., M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacillus
    and
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EMBL outstation
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       collaboration -
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Best Local
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EMBL; AP001507; BAB03874.1; -.
EMBL; D10360; BAA01192.1; -.
PIR; C44859; C44859
HSSP; P27142; 1ZIN
InterPro; IPR000850; Adenylate_kin.
Pfam; PF00406; adenylatekinase; 1.
PRINTS; PR00094; ADENYLTKNASE;
PRODOm; PD000657; Adenylate_kin; 1.
PROSITE; PS00113; ADENYLTATE_KINASE; 1.
                                                                                                                                                                                                                         J. Biol.
[2]
Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart Sgourds J., Peat N., Hayles J., Baker S., Basham D., Bowman S., Brown D., Brown S., Chillingworth T., Churcher C.M., Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KAD1_SCHPO
P33075;
                                                                                                                                                                            STRAIN-972
                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. MEDLINE-93266590;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Fungi; Ascomycota; Schizosaccharomycete Schizosaccharomycetales; Schizosaccharomycetaceae; Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-1993 (Rel. 27, Created)
01-OCT-1993 (Rel. 27, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Adenylate kinase (EC 2.7.4.3) (ATP-AMP transphosphorylase).
ADK1 OR SPAC4G9.03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              use by non-profit institutions as long a modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                     MEDLINE-21848401;
                                                                                                                                                                                                                                                "Molecular analysis of the essential gene the fission yeast Schizosaccharomyces pombus. Biol. Chem. 268:11326-11334(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Schizosaccharomyces pombe (Fission yeast)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SCHPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                          Konrad M.;
                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=4896;
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                                                                                                                       Gwilliam R.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                         PubMed=11859360;
R., Rajandream M.A.,
                                                                                                                                                                                                                                                                                                                                                 PubMed-8496185
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Pred. No. 1.1e-30;
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RESULT 15
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Best Local S
Matches 87
                      KAD1_YEAST P07170;
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Interpro; IPR000850; Adenylate_kin.
  01-APR-1988
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PRO0094; ADENYLTKNASE.
PRODOM; PD000657; Adenylate_kin; 1.
PROSITE; PS00113; ADENYLATE_KINASE; 1.
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EMBL; Z69727; CAA93553.1;
PIR; S31338; S31338.
PIR; A46718; A46718.
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87; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       220
  (Rel. 07, Created)
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                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24375 MW;
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18 ATP (BY SIMILARITY).

24375 MW; F5335A025C971D78 CRC64;
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40.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 436; DB 1; 1
Pred. No. 1.4e-30;
6; Mismatches 73;
                                             PRT;
                                             222
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EMBL; M18455, AAA66319.1; -. EMBL; U13239; AAC33143.1; -. EMBL; Y00413; CAA68471.1; -. CAA29624.1; -.
                                                                                                                                                                                                                                     "High-resolution structures of adenylate kinase from yeast ligated with inhibitor Ap5A, showing the pathway of phosphoryl transfer."; Protein Sci. 4:1262-1271(1995).
-i- FUNCTION: THIS SMALL UBIQUITOUS ENZYME IS ESSENTIAL FOR MAINTENANCE AND CELL GROWTH.
                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 3-222.
MEDLINE-86136113; PubMed-3004985;
Tomasselli A.G., Mast E., Janes W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-95192063; PubMed-7885847;
Davies C.J., Hutchison C.A. III;
"Insertion site specificity of the t.
Nucleic Acids Res. 23:507-514(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=88015563; pubMed=2821496;
proba K., Tomasselli A.G., Nielsen P.,
"The cDNA sequence encoding cytosolic (
yeast (Saccharomyces cerevisiae).";
Nucleic Acids Res. 15:7187-7187(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetales; Saccharomycetaceae; Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-1989 (Rel. 10, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Adenylate kinase cytosolic (EC 2.7.4.3) (ATP-AMP transphosphorylase).
ADK1 OR AKY1 OR AKY OR AKY2 OR YDR226W OR YD9934.11.
                                                                                  entities requires a
                                                                                            use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                           the
                                                                                                                                                                                                                                                                                                            Abele U., Schulz G.
                                                                                                                                                                                                                                                                                                                         MEDLINE=95400193; PubMed=7670369;
                                                                                                                                                                                                                                                                                                                                      X-RAY CRYSTALLOGRAPHY (1.63 ANGSTROMS).
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Proba K., Tomassel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Analysis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Biol.
                                                                                                          European Bioinformatics Institute. There are no restrictions by non-profit institutions as long as its content is in
                                                                                                                                                                              SUBCELLULAR LOCATION: Cytoplasmic.
SIMILARITY: BELONGS TO THE ADENYLATE KINASE FAMILY.
                                                                                                                                                                                                           CATALYTIC ACTIVITY: ATP SUBUNIT: MONOMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INE-88194690; PubMed-2834097; olen V., Oechsner U., Bandlow complete nucleotide sequence
                                                                                                                                    SWISS-PROT entry is copyright. It is produced through a collaboration the Swiss Institute of Bioinformatics and the EMBL outstation.
                                                                    an email to license@isb-sib.ch)
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http://www.isb-sib.ch/announce/
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Best Local Similarity 40.3%
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PDB; 2AKY; 14-NOV-95.
PDB; 3AKY; 14-NOV-95.
PDB; 1DVR; 03-APR-96.
SWISS-2DPAGE; P07170; YEAST.
SGD; S0002634; ADX1.
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Pfam; PF00406; adenylatekinase; 1.

PRINTS; PR00094; ADENYLTKNASE.

ProDom; PD000657; Adenylate_kin; 1.

PROSITE; PS00113; ADENYLATE_KINASE; 1.

Transferase; Kinase; Acetylation; ATP-binding; 3D-structure.

PROPEP 1 2 REMOVED IN MATURE FORM.
             176 YEDQTKXVLXYYQKKGVLETFSGTETNKIWPYVYAFLQTKV 216
182 YHAQTEPIVDFYKKTGI---WAGVDASQPPATVWADILNKL 219
                                            116 VPFEVIKORLTARWIHPASGRVYNIEFNPPKTVGIDDLTGEPLIOREDDKPETVIKRLKA 175
                                                                                          62 GGLVSDDIMVNMIKDELTNNPACKNGFILDGFPRTIPQAEKLDQMLKEQGTPLEKAIELK 121
                                                                                                         63 GKLIPDDVMTRLALHELKN--LTQYSWLLDGFPRTLPQAEALDRAYQ-----IDTVINLN 115
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$47475; $47475.
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222
222 AA;
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3 A
21 A
139 A
222 D
24255 MW;
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40.3%; Pred. No. 1.7e-30;
tive 50; Mismatches 72;
                                                                                                                                                                                                                                    ADENYLATE KINASE CYTOSOLIC.
ACETYLATION.
ATP (BY SIMILARITY).
A -> R (IN REF. 2).
A -> N (IN REF. 6).
D -> N (IN REF. 6).
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Search completed: March 19, 2003, 16:08:48 Job time: 314 secs

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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US-08-829-027-1
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Query Match
Best Local Similarity
Matches 227; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Hillman, Jennifer L. APPLICANT: Shah, Purvi
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  Conservative
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.3 408 2 US-08-683-007A3 600 4 US-09-134-001C2 296 1 US-08-23-454A2 491 3 US-08-923-454A2 491 3 US-08-923-0702 229 4 US-08-134-0702 229 4 US-09-134-0702 303 2 US-08-321-670-2 .3 303 4 US-09-135-252-3 .2 1663 4 US-09-132-271-1 .2 1663 4 US-09-132-334-2 .2 2089 1 US-08-418-893D2 2089 1 US-08-418-893D3 208-9 1 US-08-418-893D4 408 2 US-08-448-41 408 3 US-08-459-0481 408 3 US-08-459-0481 408 3 US-08-459-0481 408 3 US-08-459-048-
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## ALIGNMENTS

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NOVEL MITOCHONDRIAL ADENYLATE KINASE

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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 227 amino acids
                                                                                                                                                                                                                                                                                       FILING DATE:
ATTORNEY/AGENT INFORMATION:
ANAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415.855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/
FILING DATE: Herewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
COMPUTER: IBM Compat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: FastSEQ for Windows CURRENT APPLICATION DATA:
                                                                                                                             IMMEDIATE SOURCE:
                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: si
                                                                                         LIBRARY: Consensus CLONE: 2122022
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99.7%; Score 1157; DB 2; 100.0%; Pred. No. 4.3e-129; Live 0; Mismatches 0;
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                                                     Matches
                                                                             Query Match
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/225,366
                                                                                                                                                                                                                                                                 TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Hillman, Jennifer L. APPLICANT: Shah, Purvi TITLE OF INVENTION: NOVEL MITOC
                                                                                                                                             IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
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STRANDEDNESS: sir
TOPOLOGY: linear
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CITY: Palo Alto
STATE: CA
                                                                                                                   LIBRARY: Consensus
CLONE: 2122022
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                                                                                                                                                                                                                                                                                                    NAME: Billings, Lucy J. REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
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                                                               Similarity
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                                                             Score 1157; DB 3;
Pred. No. 4.3e-129;
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CURRENT FILING DATE: 1998-09-08
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EARLIER FILING DATE: 1997-03-07
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FILE REFERENCE: PZ002P1
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ER FILING DATE: 1997-08-22
ER APPLICATION NUMBER: 60/056,666
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US-08-829-027-3
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                                                                                                                                             Matches
                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 227 amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Billings, Lucy J.

REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08,
FILING DATE: Herewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
ANAME. 5111167 1707.
                                                                                                                                                                                                                                                                                                          STRANDEDNESS: sing
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 217576
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CORRESPONDENCE ADDRESS: ADDRESSE: Thomas ADDRESSE: 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM COMPANY
OPERATING SYSTEM: DOS
OPERATING SYSTEM: DOS
OPERWARE: FastSEQ for Windows Version 2.0
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CITY: Palo Alto
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                             MGASARLLRAVIMGAPGSGKGTVSSRITTHFELKHLSSGDLLRDNMLRGTEIGVLAKAFI 60
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MGASARLLRAAIMGAPGSGKGTVSSRITKHFELKHLSSGDLLRDNMLRGTEIGVLAKTFI 60
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                                                                                                                                          Conservative
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                                                                                                                                  94.0%; Score 1091; DB 2;
91.6%; Pred. No. 3e-121;
tive 10; Mismatches 9;
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	120	61 DQGKLIPDDVMTRLVLHELKNLTQYNWLLDGFPRTLPQAEALDRAYQIDTVINLNVPFEV	Db
	120	61 DQGKLIPDDVMTRLALHELKNLTQYSWLLDGFPRTLPQAEALDRAYQIDTVINLNVPFEV	Qy
	60	1 MGASAKLIKAYIMGAPOSGKGIYSSKIITHEELIHLISSUULIKUUMIKGIELIYYYANAEL 	B 5
0;	s o	Query Match 94.0%; Score 1091; DB 3; Length 227; Best Local Similarity 91.6%; Pred. No. 3e-121; Matches 208; Conservative 10; Mismatches 9; Indels 0; Ga	<b>)</b>
		LIBRARY: GenBank CLONE: 217576 S-09-225-366-3	US;
		TOPOLOGY: linear IMMEDIATE SOURCE:	
		UENCE CHARACTERISTICS: ENGTH: 227 amino acids YPE: amino acid	
		FOR SEC II	
		CATION INFORMATION: : 415-855-0555 A15-845-A166	
		RECIETRATION NUMBER: 36,749 REFERENCE/DOCKET NUMBER: PF-0256 US	
		Y/AGENT INFORMATI	
		PPLIC	
	•	SOFTWARE: FastSEQ	
		IBN	
		COMPUTER READABLE FORM: MEDIUM TYPE: Diskette	
		COUNTRY: USA ZIP: 94304	<b></b>
		STATE: CA	
		3174 Porter Drive	
		TITLE OF INVENTION: NOVEL MITOCHONDRIAL ADENYLATE KINASE NUMBER OF SEQUENCES: 5	·· ··
		CANT: Shah, Purvi	
		INFORMATION:	
		Sequence 3, Application US/U9225366 Patent No. 6001624	
		166-3	Ся
		181 EPVLEYYRKKGVLETFSGTETNKIWPHVYAFLQTKLPQRSOET	Дb
		181	Qy
	180	121 IKQRLTARWIHPGSGRVYNIEFNPPKTMGIDDLTGEPLVQREDDRPETVVKRLKAYEAQT	Дb
	180	121 IKQRLTARWIHPASGRVYNIEFNPPKTVGIDDLTGEPLIQREDDKPETVIKRLKAYEDQT	Qy
	120	61 DQGKLIPDDVMTRLVLHELKNLTQYNWLLDGFPRTLPQAEALDRAYQIDTVINLNVPFEV	Db
	120	61 DQGKLIPDDVMTRLALHELKNLTQYSWLLDGFPRTLPQAEALDRAYQIDTVINLNVPFEV	Оу

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US-08-829-027-4
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Best Local Similarity 90...
205; Conservative
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Patent No. 5856160
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SEQUENCE CHARACTERISTICS:
LENGTH: 227 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: DOS
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/829,027
FILING DATE: Herewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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APPLICANT: Shah, Purvi
TITLE OF INVENTION: NOVEL MITOCHONDRIAL ADENYLATE KINASE
NUMBER OF SEQUENCES: 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF
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MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: 415-855-0555
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                                                                    121 IKQRLTARWIHPASGRVYNIEFNPPKTVGIDDLTGEPLIQREDDKPETVIKRLKAYEDQT 180
                                                                                                                               61 DQGKLIPDDVMTRLALHELKNLTQYSWLLDGFPRTLPQAEALDRAYQIDTVINLNVPFEV 120
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STATE: CA
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                                                  IKLRLTARWIHPASGRVYNIEFNPPKTVGIDDLTGEPLIQREDDKPETVIKRLKAYEAQT
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Pred. No. 5.8e-115;
6; Mismatches 16;
                                                                                                                                                                                                                                                                           Length 227;
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RESULT 8
US-08-829-027-5
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Patent No. 6001624
                                                                                                                                                                                                                                                                                                                           Matches
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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LIBRARY: GenBa
CLONE: 450312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION: TELEPHONE: 415-855-0555
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
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STATE: CA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                              1 MGASARLLRAVIMGAPGSGKGTVSSRITTHFELKHLSSGDLLRDNMLRGTEIGVLAKAFI 60
                                                                                                                                              IKQRLTARWIHPASGRVYNIEFNPPKTVGIDDLTGEPLIQREDDKPETVIKRLKAYEDQT 180
                                                                                                                                                                                                              DQGKLIPDDVMTRLALHELKNLTQYSWLLDGFPRTLPQAEALDRAYQIDTVINLNVPFEV 120
                                                               KXVLXYYQKKGVLETFSGTETNKIWPYVYAFLQTKVPQRSQKASVTP 227
                                                                                                                                                                                                                                                            MGASGRLLRAVIMGAPGSGKGTGSSRITKHFELKHLSSGDLLRQNMLQGTEIAVLAKSFI 60
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                                                                                                                                                                                             DQGKLIPDDDMTRLALHELKNLTQCSWLLDGFPRTLPQAEALDRVYQIDTVINLNVPFEV 120
                                                                                                                                 IKLRLTARWIHPASGRVYNIEFNPPKTVGIDDLTGEPLIQREDDKPETVIKRLKAYEAQT
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RESULT 9
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                                Sequence 5, Application US/09225366 Patent No. 6001624 GENERAL INFORMATION:
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Patent No. 5856160
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SEQUENCE CHARACTERISTICS:
LENGTH: 223 amino acid
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 APPLICANT:
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LIBRARY: GenBank
CLONE: 28577
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REFERENCE/DOCKET NUMBER: PF-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
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CORRESPONDENCE ADDRESS:
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                 184
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                                                                                                                                                182 IELYKSRGVLHQFSGTETNKIWPYVYTLFSNKITPIQSKEA
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OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
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                                                                                                                                                                                                              RLSRRWIHPPSGRVYNLDFNPPHVHGIDDVTGEPLVQQEDDKPEAVAARLRQYKDVAKPV
                                                                                                                                                                                                                               RLTARWIHPASGRVYNIEFNPPKTVGIDDLTGEPLIQREDDKPETVIKRLKAYEDQTKXV 183
                                                                                                                                                                                                                                                                                                                                            ASKLLRAVILGPPGSGKGTVCQRIAQNFGLQHLSSGHFLRENIKASTEVGEMAKQYIEKS
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                 Jennifer L
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RESULT 10
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Sequence 3289, Application US/09134001C Patent No. 6380370
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LIBRARY: GenBar
LIBRARY: GenBar
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
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MEDIUM TYPE: Diskett
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NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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CORRESPONDENCE ADDRESS:
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                                                                                                          184 LXYYQKKGVLETFSGTETNKIWPYVYAFLQTKV-PQRSQKA 223
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                                                                                           IELYKSRGVLHQFSGTETNKIWPYVYTLFSNKITPIQSKEA
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                                                                                           222
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GENERAL INFORMATION:

APPLICANT: LYNN DOUCETTE-Stamm et al APPLICANT: LYNN DOUCETTE ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC TITLE OF INVENTION: MCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC TITLE REFERENCE: GTC-007

CURRENT APPLICATION NUMBER: US/09/134,001C

CURRENT FILING DATE: 1998-08-13

PRIOR APPLICATION NUMBER:

US 60/064,964

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; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-3289
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SEQ ID NO 3289
LENGTH: 222
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Best Local Similarity
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                             NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: COrley, Neil C.
TITLE OF INVENTION: DISEASE RELATED NUCLEOTIDE KINASES
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
SEQUENCE CHARACTERISTICS:
LENGTH: 194 amino acid
                                                                         REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
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                                                                                                                                                                              CLASSIFICATION: 424
PRIOR APPLICATION NUMBER:
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CITY: Palo Alto
                                                                                                                                                                                                                          APPLICATION NUMBER: U
                                                                                                                 NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
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                                                                                                                                                                     FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                    94304
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                                                                                                                                                                                                                                                                                                                                                                USA
                                                                                                                                                                                                                                                                                                                                                                                                          E: Incyte Pharmaceuticals, Inc 3174 Porter Drive
                                                            415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Guegler,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hillman, Jennifer L.
Hawkins, Phillip R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Karl
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                                                                                                                                                                                                                                          US/08/879,561
                               12:
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                                                                                                      PF-0325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 412.5; DB 4;
Pred. No. 9.7e-41;
1; Mismatches 70;
                                                                                                      S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        222;
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RESULT 12
US-08-879-561-11
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US-08-879-561-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 11, Patent No. 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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                                                                               INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: Herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 31.7.
CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                               CLASSIFICATION: 424
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Corley, TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               189 KKGVLETFSGTET-NKIWPYVYAFL 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  129 WIHPASGRVYNIEFNPPKTVGIDDLTGEPLIQREDDKPETVIKRLKAYEDQTKXVLXYYQ 188
                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM CONTROL OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      74 LDMLRDAMLAKADTSKGFLIDGYPREVKQGEEFEKKIAPPTLLLYVDAGKETMVKRLLKR 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   72 TRLALHEL -- KNLTQYSWLLDGFPRTLPQAEALDRAYQIDT-VINLNVPFEVIKQRLTAR 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14 VVGGPGSGKGTQCEKIVHKYGYTHLSTGDLLRAEVSSGSERGKKLQAIMEKGELVPLDTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12 IMGAPGSGKGTVSSRITTHFELKHLSSGDLLRDNMLRGTEIGVLAKAFIDQGKLIPDDVM 71
                                TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                       TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
                  TOPOLOGY:
                                                                  LENGTH:
                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GRGIVRQLNAEGTVDEVFQQVCSYL 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1, Application US/08879561
5817482
                                                                  194 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3: Incyte Pharmaceuticals, 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bandman,
Hillman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Corley, Neil C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                 FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hillman, Jennifer L.
Hawkins, Phillip R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Guegler, Karl
                                                                                                                                                                                                                                                                                                                                                                                                                     IBM Compatible
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                  linear
                                                                                                                                                                                                                                                                                                                                Herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                       Diskette
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                            single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DISEASE RELATED NUCLEOTIDE KINASES
                                                                                                                                                                                                                                                                                                                                                    US/08/879,561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            44; Mismatches
                                                                                                                                                                                            PF-0325 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 2.8e-18;
4; Mismatches 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 222.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -DDNEETIKKRLETYYKATEPVIAFYK 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       73
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; TYPE: amino acid
; STRANDEDNESS: Single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: CORPNOT02
; CLONE: 1484821
US-08-879-561-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                õ
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US-08-879-561-5
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                            COMPUTER: IBM COMPATIBLE
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/879,561
FILING DATE: Herewith
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
EILING DATE:
APPLICATION NUMBER:
EILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Bilings, Lucy J.
REGISTRATION NUMBER: 95,749
REFERENCE/DOCKET NUMBER: 9F-0325 US
TELECOMMUNICATION INFORMATION:
TELECHNUE: 415-855,0555
TELEPHONE: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 5, Application US/08879561 Patent No. 5817482
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Best Local Similarity
Matches 58; Conserv
                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 197 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Bandman, Olga
APPLICANT: Hillman, Jennifer L.
APPLICANT: Hawkins, Phillip R.
APPLICANT: Guegler, Karl J.
APPLICANT: Gougler, Karl J.
APPLICANT: COTIES, Neil C.
TITLE OF INVENTION: DISEASE RELATED NUCLEOTIDE KINASES
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 94304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 3174 POI
CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13 VVGGPGSGKGTQCEKIVQKYGYTHLSTGDLLRSEVSSGSARGKKLSEIMEKGQLVPLETV 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12 IMGAPGSGKGTVSSRITTHFELKHLSSGDLLRDNMLRGTEIGVLAKAFIDQGKLIPDDV- 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R--GETSGRV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RWIHPASGRVYNIEFNPPKTVGIDDLTGEPLIQREDDKPETVIKRLKAYEDQTKXVLXYY 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E: Incyte Pharmaceuticals, Inc. 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                             single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19.0%; Score 221; DB 2; Length 194; 31.2%; Pred. No. 4.2e-18; ative 33; Mismatches 63; Indels
    16.1%;
27.8%;
                                                                                                                                                                                                                                           5
  Score 187; DB 2; Length 197; Pred. No. 4.6e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----DDNEETIKKRLETYYKATEPVIAFY 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       32;
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	Qy 101ALDRAYQIDTVINLNVPFEVIKQRLTARWIHPASGRVYNIEFNPPKTVGIDDL 153	
	LPEMIRQRVIAKKLKN	
	Qy 65 LIPDDVMTRLALHELKNLTQYSWLL-DGFPRTLPQAE 100	
11,	Query Match 7.0%; Score 81; DB 4; Length 488; Best Local Similarity 24.2%; Pred. No. 0.74; Matches 48; Conservative 20; Mismatches 60; Indels 70; Gaps	
	DEDNESS: OGY: li 3-1	
	; LENGTH: 488 amino acids ; TYPE: amino acid	
	ORMATION	
	ONE: (650) 813-560 X: (650) 494-0792	
	; REGISTRATION NUMBER: 33,743 ; REFERENCE_DOCKET NUMBER: 26374-20017.00 ; TELECOMMUNICATION INFORMATION:	
	FORMATION:	
	; APPELICATION: ; FILING DATE: ; CLASSIFICATION:	
	Ä	
	IBM PC compatible SYSTEM: PC-DOS/MS-DOS	
	MEDIUM TYPE: Flop	
	ZIP: 94304-1018	
	STATE: CA	
	T:	
	CORRESPONDENCE ADDRESS:	
	TITLE OF INVENTION: A	
	APPLICANT: Colaco, Camilo	
	APPLICAN	
	APPLICANT: Tunnacliffe, APPLICANT: Welsh, David	
	GENERAL INFORMATION:	
	ence	
	RESULT 14 US-08-985-343-1	
	Db 160 SIPVIAYYETKTQLHKI 176	
	QY 180 TKXVLXYYQKKGVLETFSGTETNKI 204	
	Db 124 SA	
	QY 126 TARWIHPASGRVYNIEFNPPKTVGIDDLTGEPLIQREDDKPETVIKRLKAYEDQ 179	
	Db 76 LELLKEAMVASLGDTRGFLIDGYPREVKQGEEFGRRIGDPQLVICMDC 123	
	Qy 72 TRLALHELKNLTQYSWLLDGFPRTLPQAEALDRAYQIDTVINLNVPFEVIKQRL 125	
	:          ::    :  :   : ::     : :::   :  :: ::	
	Qy 12 IMGAPGSGKGTVSSRITTHFELKHLSSGDLLRDNMLRGTEIGVLAKAFIDQGKLIPDDVM 71	
,	Matches 5/; Conservative 3/; Mismatches 60; Indels 56; Gaps	

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RESULT 15
US-08-637-670-40
US-08-637-670-40
; Sequence 40, Application US/08637670
; Patent No. 6413521
; GENERAL INFORMATION: HOLLIPS et al.
TITLE OF INVENTION: Helminth Parasite Antigen with
TITLE OF INVENTION: Aminopeptidase-like Activity
NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: 202-783-6040
TELEPAX: 202-783-6031
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 620 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-637-670-40
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                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local S
Matches 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/637,670
FILING DATE: 26-JUN-1996
CLASSIFICATION: S36
ATTORNEY/AGENT INFORMATION:
NAME: Ernst, Barbara G,
REGISTRATION NUMBER: 30,377
REFERENCE/DOCKET NUMBER: 30,377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     316 E--WIGKVVLVQVAVPSR 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                202 NKIWPYVYAFLOTKVPQR 219
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157 -FSYSNAEATDLW 168
                                                  193 LETFSGTETNKIW 205
                                                                                                                         135 GRVYNIEFNPPKTVGIDDLTGEPLIQREDDKPETVIKRLKAY--EDQTKXVLXYYQKKGV 192
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                                                                                                                                                                                                                                                                                                                                                                                                        / Match 6.9%; Score 80.5; DB 4; Length 620; Local Similarity 23.8%; Pred. No. 1.2; nes 46; Conservative 22; Mismatches 54; Indels 7:
                                                                                                                                                                                                                              75 ALHELKNLTQYSWLLDGFPRTLPQAEALDRAYQIDTVINLNVPFEVIKQRLTARWIHPAS 134
                                                                                                                                                                                                                                                                                                                                                   25 SRITTHFELKHLSSGDL------LRDNMLRGTEIGVLAKAFIDOGKLIPDDVMTRL 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: U
                                                                                                                                                                                                 86 -----NY-FLID------VLERALKADSVAS-----SHPLS 109
                                                                                                                                                                                                                                                                                                   35 ARIVAH-ELAHQWFGDLVTMKWWDNLWLNEGFARFTE-----FIGAGQITQDDARMR- 85
                                                                                                  ---FRIDKAAEVEEAFDDITYA-----KGASVLTMLRALIGEEKHKHAVSQYLKK-- 156
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555 13TH STREET, NW
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Search completed: March 19, 2003, 16:49:22 Job time: 277 secs

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                                                                                                                                                                                                                                     Score
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Match
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Gapop 10.0 , Gapext 0.5
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AAB93066
AAB93487
AAB85885
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AAB812326
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Human secreted pro
Human polypeptide
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Human adenylate ki
                                                                                                                                                                                                                              Description
                   Human
Human
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secreted pro
polypeptide
colon cancer
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## ALIGNMENTS

AAW81101 standard; Protein; 227

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AAW81101;

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RRESULT 1
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IID AAWBII02
AC AAWG
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Hillman JL, Shah P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human mitochondrial adenylate kinase protein
                                                                                                                                                                    31-MAR-1997;
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                                                                                (INCY-) INCYTE PHARM INC
                                                                                                                                                                                                                                                        30-MAR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                        97US-0829027
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note- "Xaa is unspecified, encoded by NCA"
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RESULT 2
AAW7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The human mitochondrial adenylate kinase (HMAK) protein of 227 amino cacids) can be administered therapeutically, especially by expressing encoding polypeptides, to treat neurological disorders e.g. Alzheimer's disease, Huntington's disease, epilepsy. It can be combined with a cultible carrier in pharmaceutical compositions, which can be administered to treat such disorders. HMAK was shown to have chemical candinistered to treat such disorders. HMAK was shown to have chemical and structural homology with adenylate kinase isozyme 3 (AK3) from cow, rat and human (92, 91 and 57 % identity respectively) and was expressed in e.g. cancerous tissues, brain and neural tissues and tissues involved in inflammation and the immune response. Increased activity or expression was proposed to be associated with cancer and immunological disorders, and decreased activity/expression with the development of neurological disorders. Products of the above invention may be used in the diagnosis and treatment of the above diseases and disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Simi
Matches 227;
     02-OCT-1997;
07-MAR-1997;
07-MAR-1997;
                                                                                                                                     Homo
                                                         06-MAR-1998;
                                                                                   11-SEP-1998
                                                                                                           WO9839448-A2
                                                                                                                                                              diagnosis; neurodegenerative
                                                                                                                                                                                                                Human secreted
                                                                                                                                                                                                                                            19-JAN-1999
                                                                                                                                                                                                                                                                                              AAW74787
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human mitochondrial adenylate kinase, HMAK - useful e.g. to treat neurological disorders such as Alzheimer's and screen for antagonists for treatment of cancer or immunological disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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                                                                                                                                                                             usion
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                                                                                                                                   sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                             IKQRLTARWIHPASGRVYNIEFNPPKTVGIDDLTGEPLIQREDDKPETVIKRLKAYEDQT
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DB; AAV68223.
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                                                                                                                                                                          secreted protein;
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27; Conservative
                                                                                                                                                                                                                                                                                              standard;
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     97US-0061060.
97US-0038621.
97US-0040161.
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                                                                                                                                                                                                               protein encoded
                                                         98WO-US04493
                                                                                                                                                                         protein; testis; tumour;
cancer; central nervous ;
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                                                                                                                                                                                                                                                                                             Protein;
                                                                                                                                                                                                                                         entry)
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                                                                                                                                                               disease
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Pred. No. 2.1e-111;
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                                                                                                                                                                                                               gene
                                                                                                                                                                                                               58
                                                                                                                                                                          system;
                                                                                                                                                                                    foetal
                                                                                                                                                                                                               clone HHFHN61.
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seizure;
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07-MAR-1997;
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11-APR-1997;
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11-APR-1997;
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11-APR-1997;
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97US-0040162
97US-0040163
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97US-0040336
97US-0043311
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97US-0043313
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                                                                                                                                                                                                                                                                     This sequence represents a secreted human protein encoded by the nucleic cacid molecule designated Gene 58 from the human cDNA clone HHFHN61 (deposited as clone ATCC 97899 and ATCC 209045).

The gene can be used to generate fusion proteins by linking to the gene to a human immunoglobulin Fc portion (e.g. AAV59502) for increasing the stability of the fused protein as compared to the human protein only.

The invention relates to 186 novel genes and their fragments (nucleic acid sequences: AAV59511-V59812; amino acid sequences AAW74731-W75026) which are useful for preventing, treating or ameliorating medical conditions can be diagnosed by determining the amount of the new polynucleotides. Specific uses are described for each of the 186 polynucleotides, based on which tissues they are most highly expressed in (see AAV59511-For described for which tissues they are most highly expressed in for described for each of the 186 polynucleotides, based on which tissues they are most highly expressed in
                                                                                                                                                                                         Query Match
Best Local :
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Kyaw H,
                                                                                                                                                                                                                                    Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HUMA-) HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-SEP-1997;
05-SEP-1997;
                               121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ew isolated human genes and the secreted polypeptide(s) they encode useful for diagnosis and treatment of e.g. cancers, neurological isorders, immune diseases, inflammation or blood disorders
                                                           61
                                                                                      61
                                                                                                                                                                           Local Similarity
les 225; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1998-506364/43.
DB; AAV59568.
                                                                                                              MGASARLLRAVIMGAPGSGKGTVSSRITTHFELKHLSSGDLLRDNMLRGTEIGVLAKAFI 60
IKQRLTARWIHPASGRVYNIEENPPKTVGIDDLTGEPLIQREDDKPETVIKRLKAYEDQT 180
                                                                       DQGKLIPDDVMTRLALHELKNLTQYSWLLDGFPRTLPQAEALDRAYQIDTVINLNVPFEV 120
                                                                                                                                                                                                                                                              AAV59511 for described uses).
                                                        DQGKLIPDDVMTRLALHELKNLTQYSWLLDGFPRTLPQAEALDRAYQIDTVINLNVPFEV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Page
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Ferrie AM, Fischer CL, Florence
DW, Li Y, Moore PA, N
                                                                                                                                                                                                                                    227
                                                                                                                                                                           Conservative
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97US-0056903.
97US-0056908.
97US-0056909.
97US-0056910.
97US-0056911.
97US-0057650.
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97US-0056887.
97US-0056888.
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97US-0057761
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                                                                                                                                                                          0;
                                                                                                                                                                                      Score 1156;
Pred. No. 2
                                                                                                                                                                           Mismatches
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2.7e-111;
ches 2;
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25-APR-2000;
09-JUL-2000;
19-JUL-2000;
19-JUL-2000;
14-SEP-2000;
14-SEP-2000;
                                                       The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system disease, such as alzheimer's, parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and
                                                                                                                                                                                                                                                                                                                                              Tang
Wang
                                                                                                                                                                                                                                                                                                                                    Zhao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzhaimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAM38899
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                         specification
                                                                                                                                                                                                                                    Example
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     leukaemia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human polypeptide
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                                                                                                                                                                                                                                                                                                                                 Q, Y,
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DB; AAI58055.
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                                   The sequent
                                                                                                                                                                                                                                    3; SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                  HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                   Liu C,
Wang Z,
Zhou P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              standard;
                                    sequence
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2000US-0598042
2000US-0620312
2000US-0653450
2000US-0652191
2000US-0693036
2000US-0727344
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Wehrman T,
                                                                                                                                                                                                                                  NO 2044; 10078pp; English.
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                                    this
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Xu C, Xue
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e AJ,
RT;
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Yang Y,
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Zhang J;
                                      of
                                    the
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Sequence

Query Match Best Local

Similarity

99.6%; 99.1%;

Score Pred.

1156; No. 2

DB 22; ?.7e-111;

Length

227;

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The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprises a 3'-end sequence complementary to a polynucleotide which comprises a 5'-end sequence comprises a 1'-end sequence, where the oligonucleotide which comprises a 1'-end sequence, where the oligonucleotide comprises a 1'-end sequence, where the oligonucleotide which comprises a steast 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from these Arfinesia.
                                                                                                                                                                                                                                                                                                                                 29-JUL-1999;
27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
09-JUN-2000;
                                                                                                                                                                Claim
                                                                                                                                                                                     and/or diagnosis of the full-length cDNAs -
                                                                                                                                                                                                                                                                         Ishii
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human;
                                                                                                                                                                                             Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human protein
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                                                                                                                                                                                                                                                                                                           (HELI-)
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                                                                                                                                                                                                                                                                                      Isogai T,
                                                                                                                                                              SEQ ID 11492;
                                                                                                                                                                                                                                                                         Sugiyama
                                                                                                                                                                                                                                                                                                                                 ; 99JP-0300253.
; 2000JP-0118776.
; 2000JP-0183767.
; 2000JP-0241899.
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                                                                                                                                                                                                                                                                         Ţ,
                                                                                                                                                                                                                                                                                    Nishikawa
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Wakamatsu
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A, Nagai K,
                                                                                                                                                             ROM;
                                                                                                                                                             English
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C, Otsuki
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                                                                                                                                                                                                                                                                                   Yamamoto
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Claim

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SEQ

ID 11883;

2537pp +

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and/or diagnosis of full-length cDNAs -

tne

izing polynucleotides, particularly the 5602 ed in the specification, and for the detection abnormality of the proteins encoded by the

detection by the

Primer sets for synthesizing full-length cDNAs defined in

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RESULT 5
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Best Local S
Matches 225
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27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
09-JUN-2000;
                                                                                                                                                                                              Ota T,
Ishii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13633 to AAH18742 represent human acid sequences; and AAH13632 to AAH13632 represent oligonucleotides, all of which are used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                         28-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-FEB-2001
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, Sugiyama
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25; Conservative
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99JP-0300253.
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2000JP-0241899.
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T, Wakamatsu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein;
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99.1%;
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Pred. No. 2.7e
0; Mismatches
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A, Naga
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Nagai
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Ctsuki
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                                                                                                                                                                                                                    Yamamoto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            therapy.
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RESULT 6
AAB93487
IID AABS
XX AAB9
AC AABS
XX Huma
XX Huma
XX Huma
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XX Huma
XX Hom
QS 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention describes primer sets for synthesising 5602 (C full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the coligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence complementary to the complementary to a combination of complementary strand of a polynucleotide which comprises a 5'-end sequence, where the coligonucleotide which comprises a 3'-end sequence, where the coligonucleotide which comprises a 1'-end sequence, where the coligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and compared the sequence of the specification and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs assist without any specialised methods. AAH03166 to AAH13628 and C chab13633 to AAH13742 represent human cDNA sequences; AAB92446 to C of the present oligonucleotides, all of which are used in the exemplification cofficer of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local S
Matches 225
                         29-JUL-1999;
27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
09-JUN-2000;
                                                                                                                                                                                                                                                07-FEB-2001
                                                                                                                                                                                                                                                                                                    EP1074617-A2
                                                                                                                                                                                                                                                                                                                                                          Homo
                                                                                                                                                                                                                                                                                                                                                                                                                Human; primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB93487;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IKQRLTARWIHPASGRVYNIEFNPPKTVGIDDLTGEPLIQREDDKPETVIKRLKAYEDQT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        227
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                         99JP-0300253.
2000JP-0118776.
2000JP-0183767.
2000JP-0241899.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                          2000EP-0116126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence SEQ ID NO:12786
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K
                                                                                                                                   99JP-0248036.
                                                                                                                                                                                                                                                                                                                                                                                                                detection; diagnosis; antisense
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          227
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Pred. No. 2.7e
0; Mismatches
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2.7e-111;
                                                                                                                                                                                                                                                                                                                                                                                                           therapy;
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sequence and an oligonucleotide comprising a sequence complementary to a conjunct point of the sequence, where the oligonucleotide which comprises a 3'-end sequence, where the coligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAB95893 represent human and and sequences; AAB92436 to AAH13632 represent oligonucleotides, all of which are used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                              The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-ord primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprises at sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs -
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8; SEQ ID 12786;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Isogai T, Nis
, Sugiyama T,
227
ĀΑ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nishikawa T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2537pp +
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CD ROM;
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A, Nagai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              English
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Otsuki
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RESULT 7
AAB85885
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 30-NOV-2001
                       AAB85885;
                                            AAB85885 standard;
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                                                                                                                                                                                                                                                   1 MGASARLLRAVIMGAPGSGKGTVSSRITTHFELKHLSSGDLLRDNMLRGTEIGVLAKAFI
                                                                                                 DQGKLIPDDVMTRLALHELKNLTQYSWLLDGFPRTLPQAEALDRAYQIDTVINLNVPFEV
                                                                                                                                              IKQRLTARWIHPASGRVYNIEFNPPKTVGIDDLTGEPLIQREDDKPETVIKRLKAYEDQT
                                                                                                                                                                                                                                        MGASARLLRAVIMGAPGSGKGTVSSRITTHFELKHLSSGDLLRDNMLRGTEIGVLAKAFI
                                                                                                                                                                                            DQGKLIPDDVMTRLALHELKNLTQYSWLLDGFPRTLPQAEALDRAYQIDTVINLNVPFEV
                                                                                                                                                                                                                                                                                    225;
                                                                                                                                                                                                                                                                                    Conservative
(first
                                             Protein;
 entry)
                                             227
                                                                                                                                                                                                                                                                                    0
                                                                                                                                                                                                                                                                                    Mismatches
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                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                   Gaps
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Q 밁 Q 8 Q

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Q

Query Match

Local

Similarity

99.6%; 99.1%;

Score 1156; DB 22; Pred. No. 2.7e-111;

DB 22;

Length

227;

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adenylate

kinase 3 (AK3)-like

protein.

Adenylate kinase 3-like protein; AK3-like protein; AK3; cell morphology; MELAS; central nervous system disorder; epilepsy; skeletal muscle; muscle disease; electron transfer disorder; Leber disease; human;

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RESULT 8
ABB12326
  DXXXX
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                                                                                                                                                   Дb
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                                                                                                                                                                                                                                                       В
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                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local S
Matches 225
                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a cDNA (clone C-NT2RP2000329) encoding a novel adenylate kinase 3 (AK3)-like protein. C-NT2RP2000329 has functions of converting extracellular signals into intracellular signals and changing cell morphology. The AK3-like protein, polynucleotides and antibodies are useful in the investigation of diseases such as MELAS (cerebral accident condition with hyperlacticacidenta), central nervous system disorder, epilepsy, skeletal muscle conditions, muscle disease, electron transfer disorders, Leber disease, diabetes mellitus, Peason disease, Parkinson's disease, metabolism disorders. They are useful for developing diagnostics and treatment agents. The present sequence represents the human AK3-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-AUG-1999;
18-OCT-1999;
11-JAN-2000;
17-FEB-2000;
  11-JAN-2002
                         ABB12326
                                               ABB12326
                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nishikawa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sugiyama
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ota T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               diabetes mellitus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HELI-)
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                                                                                                                                                                                                                                                                              1 MGASARLLRAVIMGAPGSGKGTVSSRITTHFELKHLSSGDLLRDNMLRGTEIGVLAKAFI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene encoding an adenylate kinase 3-like protein, and the antibodies to it, useful for diagnosis of brain disease e.
                                                                                                                      KXVLXYYQKKGVLETFSGTETNKIWPYVYAFLQTKVPQRSQKASVTP
                                                                                                                                                                                                                    DQGKLIPDDVMTRLALHELKNLTQYSWLLDGFPRTLPQAEALDRAYQIDTVINLNVPFEV
                                                                                                                                                                                                                                                       KPVLEYYQKKGVLETFSGTETNKIWPYVYAFLQTKVPQRSQKASVTP
                                                                                                                                                                     IKQRLTARWIHPASGRVYNIEFNPPKTVGIDDLTGEPLIQREDDKPETVIKRLKAYEDQT
                                                                                                                                                                                                        DQGKLIPDDVMTRLALHELKNLTQYSWLLDGFPRTLPQAEALDRAYQIDTVINLNVPFEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2001-564737/63.
                                                                                                                                                          IKQRLTARWIHPASGRVYNIEFNPPKTVGIDDLTGEPLIQREDDKPETVIKRLKAYEDQT
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na T, Wakama
                                                                                                                                                                                                                                                                                                                                                                               of the
                                                                                                                                                                                                                                                                                                                  Similarity
                                              standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Page 34-35; 41pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  muscle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    T,
                                                                                                                                                                                                                                                                                                                                                       227
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99US-0159590.
2000JP-0118776.
2000US-0183322.
                                                                                                                                                                                                                                                                                                        Conservative
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kimura
                                                                                                                                                                                                                                                                                                                                                                               invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99JP-0248036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 disease, genetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hayashi
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                                                                                                                                                                                                                                                                                                                  99.6%;
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                                               239
                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                 Score 1156; DB 22;
Pred. No. 2.7e-111;
                                               ð
                                                                                                                                                                                                                                                                                                       Mismatches
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                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                            Length
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                                                                                                                                                                                                                                                                                                                              227;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            e.g.
                                                                                                                                                                                                                                                                                                      0;
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myeloid cell disorder; lymphoid cell disorder; asthma; arthritis; chronic inflammatory condition; proliferative retinopathy; atherosclerosis; coronary heart disease; arterial ischaemia;
cytostatic; osteopathic; vasotropic; cardiant;
antifungal; vulnerary; antiulcer.
                                                            cell culture; drug screening; gene therapy; antiinflammatory;
antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic;
                                                                                                                                                                                                                                                                                 haematopoiesis regulation; tissue growth; immunomodulator; activin; inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis; proliferation; metastasis; cancer; tumour; haematopoietic disorder;
                                                                                                                           bone disorder; osteoporosis; vascular growth disorder; tissue regeneration; wound healing; infection; immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                     secreted
                                                                                                                                                                                                                                                                                                                                                                                      cytokine;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     NO:2696
                                                                                                                                                                                                                                                                                                                                                        differentiation;
immunomodulator;
                                                                                                                           disorder;
                                                                                                                                                                                                                                                                                                                                                    growth factor;
activin;
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Homo sapiens. WO200157188-A2

09-AUG-2001.

05-FEB-2001; 2001WO-US03800

03-FEB-2000; 2000US-0496914. 27-APR-2000; 2000US-0560875.

(HYSE-) HYSEQ INC.

Tang YT, Liu C, Drmanac RT;

WPI; 2001-457740/49 N-PSDB; ABA09570.

Claim 20; Page 333; 1963pp; English

Sequences ABB10981-ABB12330 represent nucleic acids encoding them. The cinvention also relates to vectors and recombinant host cells comprising a conclectide of the invention, methods of producing the novel polypeptides, controlled against the polypeptides, methods of detecting the nucleotides or polypeptides in a sample, and methods of identifying compounds which conditions and polypeptides of the invention. Although novel, many of the polypeptides of the invention. Although novel, many of the polypeptides of the invention have homology to known proteins, thereby conditions activities, including cytokine, cell proliferation or cell differential therapeutic applications. The polypeptides of the invention may have various activities, including cytokine, cell proliferation or cell immunomodulatory activity; activine, thrombotic or thromboty conditions activities; receptor or ligand activities; or may be involved in oncogenesis, cancer cell proliferation or metastasis. Compending on their biological activities, homostatic, thrombotic or involved in oncogenesis, cancer cell proliferation or metastasis. Conditions, e.g., by protein or gene therapy. Such conditions in activities, polypeptides and nucleotides of the invention are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Such conditions include cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell conditions, e.g., by protein or gene therapy. Such conditions include cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell conditions, e.g., by protein or gene therapy. Such conditions and abnormal conditions cell and fungal infections in addition to immunomodulatory activities may be used to promote wound the provential scale and sell cultures to promote cell growth. For example, such polypeptides may be used to neuroepithelial cells manipulate stem cells in culture to give rise to neuroepithelial cells

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RESULT 9
AAN44084
XX AAN4084
XX AAN4084
XX AAN4084
XX Huma
XX Huma
XX Huma
XX Huma
XX Huma
XX Homc
XX Homc
XX Homc
XX 15-1
PR 25-1
PR 19-1
PR 
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Best Local :
                                                                                                                                                                                                                                                                   21-JAN-2000;
25-APR-2000;
09-JUL-2000;
19-JUL-2000;
03-AUG-2000;
                                                                                               Tang
Wang
Zhao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         that can be used to augment or replace cells damaged by illness, autoimmune disease or accidental damage. The polypeptides and nucleotides may also be used in the diagnosis of the above conditions, and in drug screening techniques. The present sequence represents a novel human polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                     WPI; 2001-442253/47.
N-PSDB; AAI59841.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAM40685 standard;
                                                                                                                                                                                                                                14-SEP-2000;
19-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                   26-DEC-2000; 2000WO-US34263
                                                                                                                                                                                                                                                                                                                                                                                                                          26-JUL-2001.
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 Novel nucleic acids and
                                                                                                                                                                        (HYSE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         leukaemia.
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hes 225;
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                                                                                               EY, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DQGKLIPDDVMTRLALHELKNLTQYSWLLDGFPRTLPQAEALDRAYQIDTVINLNVPFEV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        polypeptide SEQ ID NO 5616.
                                                                                                                                                                        HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                             Liu C,
Wang Z,
Zhou P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        239 AA;
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2000US-0552317.
2000US-05598042.
2000US-0620312.
2000US-0653450.
2000US-0652191.
2000US-0693036.
2000US-0727344.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                               Asundi V,
Wehrman T,
Goodrich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99.6%;
polypeptides, useful for treating disorders
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                                                                                               æ
                                                                                                                 Chen
Xu C
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                                                                                             len R, Ma
lu C, Xue
Drmanac R
                                                                                                         , S
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                                                                                               RT;
                                                                                                               Qian XB,
Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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Zhang
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                                                                                                                 ۲,
                                                                                                                                Wang
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WPI; 2001-235357/24
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RESULT 10
AAG73865
ID AAG73
XX AAG73
XX AAG73
XX Human
XX Human
XX Human
XX COLox
XX COLox
XX HOMO
PN WO200
XX HOMO
YX 29-SE
PR 29-SE
PR 03-N(
XX HUM/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 225;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; colon cancer; colorectal carcinoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C.N.S disorders.
Note: The sequence data for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        such as central nervous system injuries
                                                                                                                                                                                                    29-SEP-1999;
03-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                          WO200122920-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAG73865 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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                                                                   Ruben SM,
                                                                                                                                (HUMA-) HUMAN
                                                                                                                                                                                                                                                                                                28-SEP-2000; 2000WO-US26524
                                                                                                                                                                                                                                                                                                                                                                05-APR-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human colon cancer antigen protein SEQ ID NO:4629
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                                                                Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  239
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                                                                                                                                    GENOME SCI INC
                                                                                                                                                                                                    99US-0157137.
99US-0163280.
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99.1%;
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                                                                   Birse CE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cancer antigen;
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Pred. No. 2.9e-111;
""matches 2;
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                                                                   Rosen CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             diagnosis;
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RESULT 11
AAB12440
ID AAB12
XX AAB12
XX AAB12
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XX Human
XX Human
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XX CN124
XX CN124
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XX PA (XINI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon cancer-associated nucleic acid molecules (N) and proteins (P), where the proteins are collectively known as colon cancer antigens. The colon cancer antigens have cytostatic activity and can be used in gene therapy and vaccine production. N and P may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate P expression. For example, N and P may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of p by expressing in a patient's genome that affect the activity of p by expressing Additionally, N may be used to produce the colon cancer-associated Ps, by inserting the nucleic acids into a host cell and culturing the cell to express the proteins. N and P can be used in the prevention, diagnosis and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204 and AAB77789 represent sequences used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local S
Matches 225
 (XINH-) XINHUANGPU FUDAN GENE
                                28-SEP-1998;
                                                          28-SEP-1998;
                                                                                        05-APR-2000
                                                                                                                    CN1249340-A
                                                                                                                                                                           Human; mitochondrial GTP:AMP phosphotransferase; GTP3P; ribotide
                                                                                                                                                                                                                                                                       AAB12440;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            present invention.

N.B. Pages 666 to 682 and page 7053 of the sequence listing were missing at time of publication, meaning no sequences are present SEQ ID NO:1027 to 1052, 7921 and 7922.
                                                                                                                                                                                                        Human mitochondrial GTP:AMP phosphotransferase SEQ ID NO:4.
                                                                                                                                                                                                                                          20-OCT-2000
                                                                                                                                                                                                                                                                                                 AAB12440 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acids encoding 4277 human colon cancer-associated polypeptides, useful for preventing, diagnosing and/or treating colorectal cancers -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KXVLXYYQKKGVLETFSGTETNKIWPYYYAFLQTKVPQRSQKASVTP 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                             IKQRLTARWIHPASGRVYNIEFNPPKTVGIDDLTGEPLIQREDDKPETVIKRLKAYEDQT
                                                                                                                                                                                                                                                                                                                                                                                                                                             IKQRLTARWIHPASGRVYNIEFNPPKTVGIDDLTGEPLIQREDDKPETVIKRLKAYEDQT
                                                                                                                                                                                                                                                                                                                                                                        KPVLEYYQKKGVLETFSGTETNKIWPYVYAFLQTKVPQRSQKASVTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               225;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAH33296
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        256
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                                                                                                                                                                                                                                        (first
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                              98CN-0119439
                                                          98CN-0119439
                                                                                                                                                                                                                                                                                                Protein;
                                                                                                                                                                                                                                        entry)
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Pred. No. 3.2e
0; Mismatches
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   ENG
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   င္ပ
 LTD SHANGHA
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}.2e-111;
nes 2;
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RESULT 12
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Best Local
                                                        WPI; 2000-400718/35.
N-PSDB; AAA60585.
                                                                                      Yu L,
                                                                                                                                                                    05-APR-2000
                                                                                                                                                                                                          Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention describes a new ribotide sequence of human that is, the CDNA sequence of human mitochondrial matrix GTP:AMP phosphotransferase (GTP:P) and the encoded polypeptide. The prese sequence represents human GTP:P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Yu L,
                           Preparation of human mitochondrial matrix \mathtt{GTP} : \mathtt{AMP} phosphotransferase its encode sequence -
                                                                                                          (XINH-) XINHUANGPU FUDAN GENE
                                                                                                                             28-SEP-1998;
                                                                                                                                                 28-SEP-1998;
                                                                                                                                                                                      CN1249340-A
                                                                                                                                                                                                                             Human; mitochondrial GTP:AMP phosphotransferase; GTP3P; ribotide.
                                                                                                                                                                                                                                               AK3 protein sequence
                                                                                                                                                                                                                                                                     20-OCT-2000
                                                                                                                                                                                                                                                                                        AAB12441;
                                                                                                                                                                                                                                                                                                          AAB12441 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 4; Page 14-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Preparation of human mitochondrial matrix GTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 encode sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                       DQGKLIPDDVMTRLALHELKNLTQYSWLLDGFPRTLPQAEALDRAYQIDTVINLNVPFEV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MGAGRRLLRAVIMGAPGSGKGTVSSRISTHFELKHLSSGDLLRDNMLRGTEIGVLAKAFI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zhao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAA60582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           227 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                             98CN-0119439
                                                                                     Bi A;
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                                                                                                                                                                                                                                                                                                           Protein;
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97.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20pp; Chinese.
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Pred. No. 1.3e
1; Mismatches
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                                                                                                                                                                                                                                                                                                          227
                                                                                                          ENG
                                                                                                                                                                                                                                                                                                          A
                                                                                                          CO LTD SHANGHA.
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1.3e-108;
hes 5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        227;
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Example 2; Fig

2;

20pp; Chinese

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RESULT 13
AAB53619
ID AAB53
XX AB53
XX AB53
XX O9-MA
XX O9-MA
XX Human
XX Human
XX Human
XX Human
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XX Inerx
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XX INERX
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Best Local :
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AAC97991 to AAC98763 encode the human colon cancer associated proteins, called human colon cancer antigens, given in AAB53234 to AAB54006. The human colon cancer antigens can have cytostatic, cardioactive, muscular
                                                                                                                                                                      Colon cancer associated gene sequences, antigens, useful for the treatment, predisorders such as colon cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; colon cancer; colon cancer antigen; diagnosis; detection; identification; cytostatic; cardioactive; neuroprotective; vulne; immunomodulatory; muscular; gynaecological; gastrointestinal; nephrotropic; antiinfective; antibacterial; gene therapy; wound; neural disorder; immune system disorder; muscular disorder; reproductive disorder; gastrointestinal disorder; renal disorder
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human colon cancer antigen protein sequence SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                      (HUMA-) HUMAN GENOME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   infectious disease;
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DB; AAC98376.
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                                                                                                                                                                                                                                                                                                                                                                 CA,
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08; Conservative
                                                                                                                Page 1741-1742; 2104pp; English.
                                                                                                                                                                                                                                                                                                                                                                 Ruben
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99US-0124270.
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91.6%;
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Pred. No. 1
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                                                                                                                                                                                                prevention,
                                                                                                                                                                                                referred to vention, and
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1.5e-104;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               renal disorder
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                                                                                                                                                                                                diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     vulnerary;
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                                                                                                                                                                                                cancer
s of colon
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KGVLETFSGTETNKIWPYVYAXLQLKXHKEARK 213

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                                                                                                                                                                                                                                                            Best Local
                                                                                                                                                                                                                                                                                                                                                     neuroprotective, immunomodulatory, gynaecological, gastrointestinal, vulnerary, nephrotropic, antiinfective and antibacterial activities, and can be used in gene therapy. The colon cancer antigen polynucleotides, proteins and antibodies to the proteins are useful for the prevention, treatment and diagnosis of colon disorders, such as colon cancer. The polynucleotides may be used in diagnostics and research, such as for chromosome identification, and as hybridisation probes. The proteins may also be used to prevent diseases such as neural disorders, immune system disorders, muscular disorders, reproductive disorders, sastrointestinal disorders, wounds, renal disorders, and cardiovascular disorders. AAC98764 to AAC98772 and AAB54007 represent sequences used in the exemplification of the present
                                                                                                                                                                                                                                                                                                            Sequence
                                              121
                                                                            130
                                                                                                             61
                                                                                                                                             70
                                                                                                                                                                                          10 AVIMGAPGSGKGTVSSRITTHFELKHLSSGDLLRDNMLRGTEIGVLAKAFIDQGKLIPDD
                                                                                                                                                                            μ.
KGVLETFSGTETNKIWPYVYAFLQTKVPQRSQK 222
                                                             IHPASGRVYNIEFNPPKTVGIDDLTGEPLIQREDDKPETVIKRLKAYEDQTKXVLXYYQK
                                                                                                           AVIMGAPGSGKGTVSSRITTHFELKHLSSGDLLRDNMLRGTEIGVLAKAFIDQGKLIPDD
                                            VMTRLALHELKNLTQYSWLLDGFPRTLPQAEALDRAYQIDTVINLNVPFEVIKQRLTARW
                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                            214
                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                            Ą,
                                                                                                                                                                                                                                                         90.3%;
95.3%;
                                                                                                                                                                                                                                           Score 1048; D
Pred. No. 3.8e
3; Mismatches
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                                                                                                                                                                                                                                           8.8e-100;
ses 7;
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                                                                                                                                                                                                                                                                          Length
                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                            214:
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                                                                              189
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RESULT 14
AACH11778
ID AACH1
XX AACH1
XX AACH1
XX AACH1
XX Human
XX Human
XX Human
XX Human
XX Human
XX ALDS;
KW Cance
KW Cance
KW Cance
KW Obesi
KW anther
KW ALDS;
FT Regic
FT Regic
FT Regic
FT Regic
FT Regic
FT Regic
                                                                                                                                                                                                                                                                                                                 Human kinase; PKIN; gene therapy; adenocarcinoma; immune disorder; gout; cancer; allergy; sarcoma; leukaemia; acquired immune deficiency syndrome; AIDS; Addison's disease; microbial infection; inflammation; osteoporosis; atherosclerosis; cardiovascular disease; myocardial infarction; anaemia; myasthenia gravis; cirrhosis; cataract; growth and development disorder; seizure disorder; pulmonary embolism; Gaucher's disease; lipid disorder; lipid storage disease; Pick's disease; Tay-Sachs disease; renal disease; obesity; restorative therapy; immunomodulatory; vaccine; cardiovascular; antimicrobial; cytostatic; antiinflammatory; asthma.
                                                                                                                                                                                                                                                                                 Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human kinase (PKIN)-12 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAE11778
                                                                                                                                                                                                                         Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-DEC-2001
                                                                                                                                                                                                                                                                                 sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                          Location/Qualifiers
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Region

/note-

Domain

/note= 85..96 /note= 80..94 /note= 33..76 /note= 10..190 /note**-**9..25

"Adenylate kinase' "Adenylate kinase"

Region

Region Region

"Adenylate kinase"

kinase"

"Shikimate kinase family" "Adenylate kinase"

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                                                                                                                                                                                                        denocarcinoma, leukaemia, sarcoma, immune disorder, Addison's disease, CC acquired immune deficiency syndrome (AIDS), anaemia, asthma, allergies, CC gout, microbial infections, cardiovascular disease and/or inflammation, CC myasthenia gravis, atherosclerosis, cirrhosis, osteoporosis, myocardial CC infarction, cataract, growth and development disorder, seizure disorder, CC pulmonary embolism, Gaucher's disease, lipid disorder, lipid storage CC disease, Pick's disease, Tay-Sachs disease, renal disease and obesity. CC PKIN may be used to treat disorders associated with decreased PKIN CC expression by rectifying mutations or deletions in a patient's genome CC that affect the activity of PKIN by expressing inactive proteins or to CC supplement the patients own production of PKIN. PKIN nucleic acids may be used to produce the PKIN production of PKIN. PKIN nucleic acids may be cused to produce the PKIN production of PKIN. PKIN nucleic acids into a host cell and culturing the cell to express the protein. PKIN nucleic acid and its complementary sequences may also be used as DNA probes in CC diagnostic assays to detect and quantitate the presence of similar cultication of restorative therapy. The present sequence is human PKIN-12 crossin.
                                                                                                                                       Matches
                                                                                                                                                                      Query Match
                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   acids encoding them. PKIN is used as vaccine and in gene therapy. PK used in the prevention, diagnosis and treatment of diseases cancers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 138-139; 166pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Yue H, Gandhi AR, Tribouley CM, Kearney L, Griffin JA, Nguyen DB;
Bandman O, Lu DAM, Lal P, Burford N, Khan K, Yao MG;
Patterson C, Burrill JD, Marcus GA, Zingler KA, Recipon SA, Lu Y;
Policky JL, Thornton M, Tang YT, Hafalia A, Elliott VS, Baughn MR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human kinases and nucleic acids, useful for preventing diagnosing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Policky JL, Thornton N
Walsh RT, Ramkumar J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-APR-2000;
05-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Region
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   62
                                   64
                                                                                                                                                      Loca.
                                                                      N
                                                                                     present invention relates to human kinases (PKIN) and the nucleic
LUPPHVITRLMMSELENRRGQHWLLDGFPRTLGQAEALDKICEVDLVISLNIPFETLKD
              KLIPDDVMTRLALHELKNLTQYSWLLDGFPRTLPQAEALDRAYQIDTVINLNVPFEVIKQ 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2001-611740/70.
DB; AAD18827.
                                                                ASKLLRAVILGPPGSGKGTVCQRIAQNFGLQHLSSGHFLRENIKASTEVGEMAKQYIEKS
                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cancers, inflammation and immune
                                                                                                                                                                                                        224 AA;
                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2000US-203505P.
2000US-205564P.
2000US-207739P.
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2000US-202339P
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107..124
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                                                                                                                                                     56.48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Adenylate kinase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Shikimate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Adenylate kinase motif"
                                                                                                                              Score 655; DB 22; pred. No. 1.9e-59;
                                                                                                                                     38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          kinase family"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Au-young J, Hillman JL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             disorders
                                                                                                                                                                   Length
                                                                                                                                     Indels
                                                                                                                                   2
                                                                                                                                 Gaps
                                                                61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PKIN is
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ABG23968
ID ABG2
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                                                                                                       CC polypertide (II) sequences. (I) is useful as hybridisation probes, CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome CC and gene mapping, and in recombinant production of (II). The CC polynucleotides are also used in diagnostics as expressed sequence tags CC for identifying expressed genes. (I) is useful in gene therapy techniques CC (II). (II) is useful for generating antibodies against it, detecting or CC quantitating a polypeptide in tissue, as molecular weight markers and as a foot disorders involving (II). (II) and its binding partners are useful for treating CC imaging of sites expressing (II). (I) and (II) are useful for treating CC disorders involving aberrant protein expression or biological activity. CC The polypeptide and polynucleotide sequences have applications in CC diagnostics, forensics, gene mapping, identification of mutations CC responsible for genetic disorders or other traits to assess biodiversity and oacid sequences. ABG00010-ABG30377 represent novel human CC diagnostic amino acid sequences of the invention of the portnered content of the portnered content of the portnered content of the fortune of the portnered content of the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   밁
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                                                                  Note: The sequence data for this patent did not appear in the specification, but was obtained in electronic format directly
Sequence
                                            at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to isolated polynucleotide (I) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31-MAR-2000;
23-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-MAR-2001; 2001WO-US08631.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; chromosome mapping; gene mapping; gene therapy; forensic;
food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-FEB-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABG23968;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2001-639362/73.
DB; AAS88155.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IELYKSRGVLHQFFRNRRRTKIWPYVYTTFLNKITPIQSKEA
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  335 AA;
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2000US-0649167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of mutations to assess
                                                                       from WIF
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Query Match Best Local Similarity

54.9%;

Score Pred.

639; DB 22; No. 1.5e-57;

Length

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Title:
Perfect score:
Sequence:
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Maximum Match 10
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Maximum DB seq length: 2000000000
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Pred. No. is the number of results predicted by chance to have a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        March 18, 2003, 19:59:24; Search time 31295 Seconds (without alignments) 794.178 Million cell updates/sec
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854
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1: gb_ba:*
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Gapop 10.0 , Gapext 1.0
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

RESULT 1 AR027227 LOCUS DEFINITION ACCESSION VERSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL FEATURES	CC	Result
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            CAGTTACTCCATGAGGAGAAATGTGTGTAACTATTAATAGTAAGATGGGCAAACCTCCTA
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Hillman,J.L. and Shah,P.
Mitochondrial adenylate kinase
Patent: US 6001624-A 2 14-DEC-1999;
Location/Qualifiers
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BC013771
BC013771.1 GI:
MGC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clone distribution: MGC clone distribution information through the I.M.A.G.E. Consortium/LLNL at: http://imag Series: IRAK Plate: 26 Row: o Column: 3
This clone was selected for full length sequencing bec passed the following selection criteria: matched mRNA Location/Qualifiers
1. 1667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lou Staudt
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genom
Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: villalon@bcm.tmc.edu.
Villalon, D.K., Luna, R.A., Hale, S.M., Hul:
A.M., Holloway, M., Telford, B, Hodgson, A.
Muzny,D.M., Gibbs,R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (04-SEP-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                        /product "Unknown (protein for MGC:21124)"
/protein_id "AAH13771.1"
/protein_id "AAH13771.1"
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/translation = "MGA
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/db_oxref="taxon:9606"
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/clone_lib="NIH_MGC_85"
                                                                                                                                                                                                                                                                                                                                            /note="Vector:
                                                                                                                                                                                                                                                                                                    /codon_start=1
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                    Score 835.2; DB 9;
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                                                          oligo capping; fis (full insert sequence). Homo sapiens placenta cDNA to mRNA, clone_lib:PLACE1
                                                                                                                                     AK001951 1701 bp mRNA linear PRI 01-AUG-2002 Homo sapiens cDNA FLJ11089 fis, clone PLACE1005305, highly similar to GTP: AMP PHOSPHOTRANSFERASE MITOCHONDRIAL (EC 2.7.4.10).
                                                                                                  AK001951
AK001951.1 GI:7023533
                  Homo sapiens
                                     clone: PLACE1005305
Metazoa; Chordata;
Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (16-FEB-2000) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986) NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction, 5'- & 3'-end one pass sequencing and clone selection: Helix Research Institute (supported by Japan Key Technology Center etc.) and Department of Virology, Institute of Medical Science, Institute of Virology, Institute of Medical Science,
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2 (bases 1 to 1701)
Isogai, T. and Otsuki, T.
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/db_xref="01:7023534"
/translation="MGASARLERAVIMGAPGSGKGTVSSRITTHFELKHLSSGDLLRD
/translation="MGASARLERAVIMGAPGSGKGTVSSRITTHFELKHLSSGDLLRD
NMLRGTEIGVLAKAFIDGGKLIPDDVMTRLALHELKNLTQYSWLLDGFPRTLPQAEAL
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DRAYQIDTVIKKLKAYEDQTKPVLEYYQKKGVLETFSGTETNKIWPYVYAFLQTKVPQ
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/codon_start=1
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/clone_lib="PLACE1"
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/db_xref="taxon:9606"
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                                                                                    L Unpublished
E 2 (bases I to 2642)
E 2 (bases I to 2642)
(S Isogal, T. and Otsuki, T.

Direct Submission
Submitted (16-FEB-2000) Takao Isogai, Helix Research Institute,
Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
(E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)

NEDO human cDNA sequencing project supported by Ministry of
International Trade and Industry of Japan; CDNA full insert
sequencing: Research Association for Biotechnology; cDNA library
construction, 5'- & 3'-end one pass sequencing and clone selection:
Helix Research Institute (supported by Japan Key Technology Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTGGNATATTACCAGAAAAAAGGGGTGCTGGAAACATTCTCCGGGAACAGAAACCAACAAG
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/db_xref="taxon:9606"
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nmlrgteigvlakafidQgklipddvmtrlalhelknltqyswlldgfprtlpqaeal
dravqidtvinlnvpfevikQrltakwihpasgrvynlefnppktvgidbltgbbliq
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/db_xref="GI:7022877"
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FI SHIZUKO ISHII, TOMOYASU SUGIYAMA, AI WAKAMATSU, KEIICHI NAGAI, PI

FI SHIGEO IHARA, HIROKI NAKAE, TETSUO NISHIKAWA, KOICHI KIMURA PC

C12N15/54, C12N9/12, C12N1/21, C12P21/02, C07K16/40, C12Q1/68, PC

C12N1/00,

PC 601N33/15//
PC 601N3/15//
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1 (bases 1 to 2394)
Ota,T., Isogai,T., Hayashi,K., Saito,K., Yamamoto,J., Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K., Otsuk,T., Ihara,S., Nakae,H., Nishikawa,T. and Kimura,K.
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/db_xref="taxon:9606"
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                                                      Isogai,T., Ota,T., Hayashi,K., Sugiyama,T., Otsuki,T., Suzuk Nishikawa,T., Nagai,K., Sugano,S., Shiratori,A., Sudo,H., Wagatsuma,M., Hosolri,T., Kaku,Y., Kodaira,H., Kondo,H., Sugawara,M., Takahashi,M., Chiba,Y., Ishida,S., Murakawa,K., Ono,Y., Takiguchi,S., Watanabe,S., Kimura,K., Murakami,K., Ishii,S., Kawai,Y., Saito,K., Yamamoto,J., Wakamatsu,A., Ishii,S., Kawai,Y., Saito,K., Masuho,Y., Ninomiya,K. and Iwayana, Nakamura,Y., Nagahari,K., Masuho,Y., Ninomiya,K. and Iwayana,
                                                                                                                                                                                     AK027534.1 GI:14042280 oligo capping; fis (full insert sequence). Homo sapiens teratocarcinoma cell_line:NT2 clone_lib:NT2RP2 clone:NT2RP2000329.
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            2 (bases 1 to 2394)
Isogai, T. and Otsuki, T.
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                                             cDNA sequencing project
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                                              GAGTCTATAACATTGAATTCAACCCTCCCAAAACTGTGGGCATTGATGACCTGACTGGGG
                                                          GAGTCTATAACATTGAATTCAACCCTCCCAAAACTGTGGGCATTGATGACCTGACTGGGG
                                                                                           CCAAGGCTTTCATTGACCAAGGGAAACTCATCCCAGATGATGTCATGACTCGGCTGGCCC
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    Conservative
                                                                                                                                                      /protein_id="Bab55183.1"
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DRAYQIDTVIKLNVPFEVIKQRLTARWIHPASGRVYNLEFNPKTVGIDDLTGEPLIQ
REDDKPETVIKRLKAYEDQTKPVLEYYQKKGVLETFSGTETNKIWPYVYAFLQTKVPQ
                                                                                                                                                                                                                                                                                                                                                   precursor cells after 2-weeks retinoic acid induction."
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/cell_line="NT2"
/cell_type="teratocarcinoma"
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Sugiyama T., Wakamatsu A., Nagai K., Otsuk T., Ihar
Nishikawa T., Kimura K.;
"Novel genes encoding adenylate kinase 3(AK3) like
Patent number JP03074939-T/1, 30-JAN-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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08-FEB-2002
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J P 03074939-T/1

D 30-JAN-2001

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F 28-JUL-2000 JP 2000005066

F 28-JUL-1999 JP 99P 248036,27-AUG-1999 JP 99P 300253

R 11-JAN-2000 JP 00P 118775,18-CCT-1999 US 60/159590

R 11-FEB-2000 US 60/18372

I TOSHIO CTA,TAKAO ISCGAI,KOJI HAYASHI,KAORU SAITO,

I JUNICHI YAMAMOTO,

I SHIZUKO ISHII,TOMOYASU SUGIYAMA,AI WAKAMATSU,KEIICHI NAGAI,

TETSUJI OTSUKI,

SHIGEO IHARA,HIROKI NAKAE,TETSUO NISHIKAWA,KOICHI KIMURA

C C12N155/54,C12N9/12,C12N1/21,C12P21/02,C07K16/40,C12Q1/68,
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                              ATTAAACAACGCCTTACTGCTCGCTGGATTCATCCCGCCAGTGGCCGAGTCTATAACATT
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                                                                                                                                                                                                                                                                                                                                                                                                                   673;
                                                                                                                                                                                                                                                       Submitted (25-DEC-1998) Takafumi Noma, Yamaguchi University School of Medicine, Department of Biochemistry; 1144 Kogushi, Ube, Yamaguchi 755-8505, Japan (E-mail:tnoma@po.cc.yamaguchi-u.ac.jp, Tel:81-836-22-2215, Fax:81-836-22-2315)
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hAK3alpha; adenylate kinase 3 alpha
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="adenylate kinase 3 alpha"
/protein_id="adenylate kinase 3 alpha"
/protein_id="BAA87913.1"
/db_xref="G::6518533"
/translation="MGASGRILRAVIMGAPGSGKGTVSSRITTHFELKHLSRGDLLRD
NMLRGTEIGVLAQAFIQQGKLIPDYVTTRLALHELKNLTQYSWLLDGFPTTLPQAEAL
DRAYQIDTVINLNVPFEVIKQRLTARWIHPASGRVYNIEFNPPKTVGIDDLTGEPLIQ
REDDKFETVIKRLKAYEDQTKPVLEYYQKKGVLETFSGTETNKIWPYVYAFLQTKVPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RSQKASVTP"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tissue_type="liver"
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Pred. No. 1.4e-155;
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AGAAATTGGCGTGTTAGCCAAGGCTTTCATTGACCAAGGGAAACTCATCCCAGATGATGT
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Li,Y., Peng,Y., Jiang,Z.,
A novel gene expressed in
unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene for AF183419
                                                                                                                                                                                                                                                                                                                                                       Submitted (03-SEP-1999) Chinese National Human Genome Center at Shanghai, 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai 201203, P. R. China
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo
                                                                                                                                                                                                                                                                                                                                                                                           Peng,Y., GU,W., Huang,C.,
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                          Similarity
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                                                                                                                                                    /evidence=not_experimental
/product="GTP:AMP phosphotransferase"
/protein_id="AAG09688.1"
/db_xref="GI:996377"
/db_xref="GI:9963777"
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LKAYEDQTKPVLEYYQKKGVLETFSGTETNKIWPYVYAFLQTKVPQRSQKASVTP"
a 273 c 282 g 470 t
                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
1. .1539
                                                                                                                                                                                                                                                                    /note="MGAPT protein"
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                                                                                                                                                                                                                                                                                           /tissue_type="pheochromocytoma"
                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                         76.5%;
99.7%;
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Submitted (04-JUL-2002) Takao Isogai, FLJ Project(HRI Team); 2-6-7 Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986) KEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and
                                                                                                                                                                                                                                                                                                                                                                    Oshima,A., Takahashi-Fujii,A., Tanase,T., Imose,N., Takeuchi,K., Arita,M., Musashino,K., Yuuki,H., Hara,H., Sugiyama,T., Irie,R., Otsuki,T., Sato,H., Wakamatsu,A., Ishii,S., Yamamoto,J., Isono,Y., Kawal-Hio,Y., Saito,K., Nishikawa,T., Kimura,K., Yamashita,H., Matsuo,K., Nakamura,Y., Sekine,M., Kikuchi,H., Kanda,K., Wagatsuma,M., Murakawa,K., Kanehori,K., Sugiyama,A., Kawakami,B., Suzuki,Y., Sugano,S., Nagahari,K., Masuho,Y., Nagai,K. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AK098205.1 GI:21758171 oligo capping; fis (full insert sequence). Homo sapiens uterus cDNA to mRNA, clone_lib:UTERU2
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Mammalia; Eutheria; Primates;
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                                                                                                                                                                                                                                                                                                                            human cDNA sequencing
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                                                                                                                                           GCTTTTCCTAAGACTTCTAGTATGTATGAATTCTTTGAAAATTATATTACTTTTA 854
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GTP:AMP phosphotransferase; adenylate kinase.
Bovine liver, cDNA to mRNA, clones
lambda-bcAK3-{1-1.2-2,2-1,2-8,3-5,3-9,2-3,2-7}.
                                                           Bovine mitochondrial M25757
Bos taurus
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/tissue_type="uterus"
/clone_lib="UTERU2"
/note="cloning vector: page 142 c 622 g 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
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99.7%;
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Eukaryota;

Metazoa; Chordata; Craniata; Vertebrata;

Euteleostomi;

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                                       TTATGAAGACCAAACAAAGNCAGTCCTGGNATATTACCAGAAAAAAGGGGTGCTGGAAAC
                                                                                                                              CCGTGTCTACAACATCGAGTTCAACCCTCCCAAAACCATGGGAATTGATGATCTGACTGG
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ATTCTCCGGAACAGAAACCAACAAGATTTGGCCCTATGTATATGCTTTCCTACAAACTAA
                         TTATGAAGCCCAAACAGAGCCTGTCCTGGAGTACTACAGGAAAAAAAGGGGTGTTGGAAAC
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Cloning and characterization of cDNA for mi
phosphotransferase of bovine liver
J. Biol. Chem. 264 (32), 19192-19199 (1989)
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NMLRGTEIGVLAKTFIDQGKLIPDDVMTRLVLHELKNLTQYNWLLDGFPRTLPQAEAL
DRAYQLDTVINLNVPEEVIKQRLTARWIHPGSGRVYNIEFNPFRTMGIDDLTGEPLVQ
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/db_xref="GI:163528"
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/db_xref="taxon:9913"
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for mitochondrial GTP:AMP
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                               GCACCGTGTCTTCGCGTATCATCAAGCATTTCGAGCTGAAGCACCTCTCCAGCGGGGAC
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Oryctolagus cuniculus adenylate
AF417508
AF417508.1 GI:15778673
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 (bases 1 to 725)
Brochiero, E. and Lapointe, J.Y
Direct Submission
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Oryctolagus cuniculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (10-SEP-2001) Department of Physiology, Universite de Montreal, PO BOX 6128, Succursale Centre-ville, Montreal, QC H3C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biochim. Biophys. Acta 1510 (1-2),
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                                                                                                                                                                                                                                                                                 /product="adenylate kinase 3"
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/db_xref="Gi:15778674"
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DRAYQLDTVIKLNVPFEVIKQRLTARWIHPASGRVYNLEFNPBKTVGLDDLTEEPPLO
REDDKPETVIKRLKAYEAQTEPVLEYYRKKGVLETFSGTETNKIRPNVYAFLQTKIPE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Oryctolagus cuniculus"
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Mus musculus, ac
IMAGE:4217820, n
BC016432
                                                                               NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium
DNA Sequencing by: Baylor College of Medicine Human
                                                                                                                                                                                     Submitted (31-OCT-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
Gunaratne, P.H., Garcia, A.M., Lu, Yoon, V.S., Kowis, C.R., Lawrence, Richards, S., Gibbs, R.A.
                                                                                                                                                                                                                                                      Eukaryota; Metazoa;
Mammalia; Eutheria;
1 (bases 1 to 1850)
                                                                                                                                                                                                                                                                                           Mus
                                 Web site: http://www.hgsc.bcm.tmc.edu/cdna/Contact: amg@bcm.tmc.edu
                                                              Center code: BCM-HGSC
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           Hulyk, S.W.,
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GAGCTTATCAGATCGACACAGTGATTAACCTGAATGTGCCCTTTGAGGTCATTAAACAAC
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This clone was selected for full length sequencing because it passed the following selection criteria: GenomeScan gene prediction, Similarity but not identity to protein.
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REDDKPETVIKRLKAYEAQTEPVLQYYQKKGVLETFSGTETNKIMPHVYSFLQTKVPE
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/product="adenylate kinase
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/db_xref="GI:1674173"
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/db_xref="taxon:10090"
/map="FVB/N"
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/clone_lib="NCI_CGAP_Co24"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="MGC:25636 IMAGE:4217820"
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This clone was selected for full length sequencing because it passed the following selection criteria: GenomeScan gene prediction, Similarity but not identity to protein.
                                                                                                                                                                                                                                                                                               Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
Web site: http://www.nisc.nih.gov/
Contact: nisc_mgc@nhgri nih.gov
Akhter.N. Ayele,K. Beckstrom-Sternberg,S.M. Benjamin,B.,
Blakesley,R.W. Bouffard,G.G. Breen,K. Brinkley,C. Brooks,S.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
Maduro,O.L., Mastello,C., Maskeri,B., Mastrian,S.D.,McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green,E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tissue Procurement: Gilbert Smith, Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: National Institutes of Health Intramural

Sequencing Center (NISC),

Gaithoreburg Maryland.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (07-DEC-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 1860)
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BC019174.1 GI:17512427
MGC.
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old mouse. Taken by biopsy."
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CTGTTACTCCCTGAAGAG
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Listeria innocua c	ABQ67196	24	684707	11.8	101	4
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Bacillus clausii g	ABK77752	24	637	۲.	101.2	2
Klebsiella pneumon	AAS53899	23	645	2		=
Arabidopsis thalia	ABN98716	24	894		104	ö
thal	AAC49022	21	1017	12.5		39
aı	AAF28547	22	89047		107.2	8
Arabidopsis thalia	AAC37085	21	1023	12.7		37
8	AAS54207		648	ω.	•	36
Salmonella typhi D	AAS55982		645	ω		35
emophi	AAS53274		645	14.0		34
Neisseria meningit	AAF21608		349980	15.4		ω
N. meningitidis pa	AAA81463		78845	15.4	131.4	ະ
-	ABK38942		568	9	~	
	ABL11426		3454		0	ö
e	ABL11427		699		190.2	
	AAD18827		912	6	CD.	8
Human immune/haema	AAK84484		8163	28.2	241	
H	AAL05749		8163	8	241	
Human reproductive	AAL05747		1947	8	241	25
neurobla	AAI97292		787	8	241	
Kidney cancer rela	ABL68575		1707	9	255	
cancer	ABL66518		1707	9	255	
cancer	ABL65257		1707	9.	255	
cancer rela	ABL64778		1707	७.	255	
Gene #3752 used to	ABN97254		1707	9.	255	
Human neuroblastom	AAI94359		881	۲,	366	8
A encoding no	AAS27219		2238		92	17
AK3 nucleotide seq	AAA60585		684	σ.	71	9
CDNA	AAH07675		803	7.	78	5
CDNA	AAH05788		639	9.	95	4
cDNA clone	AAH06376		851	7.	58	ω
_	3	21	733			2
mitochondr	AAA60582	21	751	85.5	29	Ξ
Human adenylate ki	AAH47197	22	2394	5	-	5

## ALIGNMENTS

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AAV6823
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                                          31-MAR-1997;
                                                                                                                                    30-MAR-1998;
                                                                                                                                                                                                                               08-OCT-1998
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                                               97US-0829027
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                                                                                                                                                                                                                                                                                                                                                                                                /*tag= a
/product= "Mitochondrial adenylate kinase"
/product= "Mitochondrial adenylate kinase"
/transl_except= (pos:594..596,aa:Xaa)
/transl_except= (pos:603..605,aa:Xaa)
/note= "Xaa is unspecified"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The human mitochondrial adenylate kinase (HMAK) (854bp) gene encodes a protein of 227 amino acids ) can be administered therapeutically. Cespecially by expressing encoding polypeptides, to treat neurological disorders e.g. Alzheimer's disease, Huntington's disease, epilepsy. It can be combined with a suitable carrier in pharmaceutical compositions, which can be administered to treat such disorders. HMAK was shown to have chemical and structural homology with adenylate kinase isozyme 3 (AK3) from cow, rat and human (92, 91 and 57 % identity respectively) and was expressed in e.g. cancerous tissues, brain and neural tissues and tissues involved in inflammation and the immune response. Increased activity or expression was proposed to be associated with cancer and immunological disorders, and decreased activity/expression with the development of neurological disorders. Products of the above invention may be used in the diagnosis and treatment of the above
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local S
Matches 854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human mitochondrial adenylate kinase, HMAK - useful e neurological disorders such as Alzheimer's and screen antagonists for treatment of cancer or immunological (
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                                                                              CGTCGCGCATCACTACACACTTCGAGCTGAAGCACCTCTCCAGCGGGGACCTGCTCCGGG
AACTCATCCCAGATGATGTCATGACTCGGCTGGCCCTTCATGAGCTGAAAAAATCTCACCC
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                                                                                                                                                                      AGTATAGCTGGCTGTTGGATGGTTTTCCAAGGACACTTCCACAGGCAGAAGCCCCTAGATA
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27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
                                                                                                                                                                                                                                Claim
                                                                                                                                                                                                                                                                       Primer sets for synthesizing polynucleotides, particularly toull-length cDNAs defined in the specification, and for the and/or diagnosis of the abnormality of the proteins encoded full-length cDNAs -
                                                                                                                                                                                                                                                                                                                                                                               WPI;
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, Sugiyama
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; 99JP-0300253.
; 2000JP-0118776.
; 2000JP-0183767.
; 2000JP-0241899.
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T, Wakamatsu
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A, Nagai K
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The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the computementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprises a 3'-end sequence, where the polynucleotide which comprises a 3'-end sequence, where the

a combination

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                                                                                                                                                                                   CCTCCCAAAACTGTGGGCATTGATGACCTGACTGGGGAGCCTCTCATTCAGCGTGAGGAT
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                                                                                                                                                                                                                                                                                 CGCCTTACTGCTCGCTGGATTCATCCCGCCAGTGGCCGAGTCTATAAACATTGAATTCAAC
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 TCAGTTACTCCATGAGGAGAAATGTGTGTAACTAGTAAAGATGGGCAAACCTCCT
                                                                                                   ATTTGGCCCTATGTATATGCTTTCCTACAAACTAAAGTTCCACAAAGAAGCCAGAAAGCT
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                                      TCAGTTACTCCATGAGGAGAAATGTGTGTAACTATTAATAGTAAGATGGGCAAACCTCCT
                                                                                      ATTTGGCCCTATGTATATGCTTTCCTACAAACTAAAGTTCCACAAAGAAGCCAGAAAGCT
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970S-0040161

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970S-0040334

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970S-0043311

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970S-0043313

970S-0043568

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970S-0043673

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23-MAY 1997
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2-AUG-1997;
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SM,
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DB; AAW74788.
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1, Shi Y,
                                                                   DP, Brewer LA, ()
Ferrie AM, Fische
Lafleur DW, Li Y,
Shi Y, Soppet I
   diagnosis
            human genes
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970S-0056875

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Fischer CL, Florence
, Li Y, Moore PA, Ni
Soppet DR, Young PE, Y
es and the secreted polypeptide(s) they encode and treatment of e.g. cancers, neurological
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ce KA, Greene JM,
Ni J, Olsen HS,
Yu GL, Zeng Z;
                                                                                      JM,
                                                                                                   Endress
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n CA;
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CC This sequence represents a nucleic acid molecule designated Gene 58 from CC the human cDNA clone HHFHN61 (deposited as clone ATCC 97899 and ATCC 209045) which encodes a secreted human protein. The gene can be used to CC generate fusion proteins by linking to the gene to a human cC immunoglobulin Fc portion (e.g. AAV59502) for increasing the stability of CC the fused protein as compared to the human protein only.

CC The invention relates to 186 novel genes and their fragments (nucleic cC acid sequences: AAV59511-V59812; amino acid sequences AAW74731-W75026) CC which are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Also, pathological conditions CC can be diagnosed by determining the amount of the new polypeptides in a CC sample or by determining the amount of the new polypeptides. Specific uses are described for each of the 186 CC polynucleotides, based on which tissues they are most highly expressed in CC (see AAV59511 for described uses).
  Sequence 1751 BP; 531 A; 353 C; 379
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G;
  485
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Τ;
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3 other;
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Query Match Best Local Sim Matches 848;

Local Similarity

97.8%; 99.2%;

Conservative

0, Score Pred.

Mismatches 835.2; No. 3.5 No.

2; DB 19; 3.5e-236; nes 6;

Indels Length

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δÃ Ş Qy В δÃ B В 망 밁 Q 밁 δÃ 밁 δÃ В δÃ 밁 δÃ 밁 δÃ В Q В QY 704 660 644 600 584 540 524 480 464 420 404 360 344 300 284 240 224 180 164 120 104 60 44 ب GATAAACCAGAGACGGTTATCAAGAGACTAAAGGCTTATGAAGACCAAACAACAAGNCAGTC CAGTATAGCTGGCTGTTGGATGGTTTTCCAAGGACACTTCCACAGGCAGAAGCCCTAGAT GCCANGCCCAAAGCCCTGGTACCCGCGGCGGTG-GGGCCTCAGTCTGCGGCCATGGGGGCG ATTTGGCCCTATGTATATGCTTTCCTACAAACTAAAGTTCCACAAAGAAGCCAGAAAGCT CCTCCCAAAACTGTGGGCATTGATGACCTGACTGGGGAGCCTCTCATTCAGCGTGAGGAT AAACTCATCCCAGATGATGTCATGACTCGGCTGGCCCTTCATGAGCTGAAAAATCTCACC GACAACATGCTGCGGGGCACAGAAATTGGCGTGTTAGCCAAGGCTTTCATTGACCAAGGG TCGTCGCGCATCACTACACACTTCGAGCTGAAGCACCTCTCCAGCGGGGACCTGCTCCGG TCCGCGCGGCTGCTGCGAGCGGTGATCATGGGGGCCCCGGGCTCGGGCAAGGGCACCGTG ATTTGGCCCTATGTATATGCTTTCCTACAAACTAAAGTTCCACAAAGAAGCCAGAAAGCT AGAGCTTATCAGATCGACACAGTGATTAACCTGAATGTGCCCTTTGAGGTCATTAAACAA **AAACTCATCCCAGATGATGTCATGACTCGGCTGGCCCTTCATGAGCTGAAAAATCTCACC** GACAACATGCTGCGGGGCACAGAAATTGGCGTGTTAGCCAAGGCTTTCATTGACCAAGGG 659 643 599 583 479 463 419 119 703 523 403 359 343 299 179 163 103 59 283 239 223

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AAB95893 represent human amino acid sequences; and AAH13629 to represent oligonucleotides, all of which are used in the exempl of the present invention.

exemplification

AAH13632

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ARESULT 4
AAHL1477
ID AAHH1
XX AAHL147
AC AAHL1
XX AAHL1
XX Huma
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XX Huma
XX Huma
XX Huma
XX EP10
XX 29-J
PR 27-4
PR 11-J
PR 11
to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the coligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end complementary to a polynucleotide comprises a 3'-end sequence complementary to a polynucleotide which comprises a 3'-end sequence complementary to a coligonucleotide comprises a 1'-end sequence, where the coligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length CDNAs easily without any specialised methods. AAH03166 to AAH13628 and CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to
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27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
09-JUN-2000;
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Ishii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and/or diagnosis of the
full-length cDNAs -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim
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Sugiyama
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99JP-0300253.
2000JP-0118776.
2000JP-0183767.
2000JP-0241899.
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T, Wakamatsu
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ı A, Nagai K,
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Otsuki
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                                                                     CTGGNATATTACCAGAAAAAAGGGGTGCTGGAAACATTCTCCGGAACAGAAACCAACAAG
                                                                                                                                                                              CCTCCCAAAACTGTGGGCATTGATGACCTGACTGGGGAGCCTCTCATTCAGCGTGAGGAT
                                                                                                                                                                                                                                                                                                                                   CAGTATAGCTGGCTGTTGGATGGTTTTCCAAGGACACTTCCACAGGCAGAAGCCCTAGAT
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          ATTATATTACTTTTA
                                           CGCCTTACTGCTCGCTGGATTCATCCCGCCAGTGGCCGAGTCTATAACATTGAATTCAAC
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ATTATATTACTTTTA
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RESULT 5 AAH33296

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                                                                                                                                                                                                                                                       CC AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon CC cancer-associated nucleic acid molecules (N) and proteins (P), where CC the proteins are collectively known as colon cancer antigens. The colon CC cancer antigens have cytostatic activity and can be used in gene CC therapy and vaccine production. N and P may be used in the prevention, CC diagnosis and treatment of diseases associated with inappropriate P CC expression. For example, N and P may be used to treat disorders CC associated with decreased expression by rectifying mutations or deletions CC in a patient's genome that affect the activity of P by expressing CC inactive proteins or to supplement the patients own production of P. CC Additionally, N may be used to produce the colon cancer-associated Ps, CC by inserting the nucleic acids into a host cell and culturing the cell CC by inserting the proteins. N and P can be used in the prevention, diagnosis and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204 CC and AAB77789 represent sequences used in the exemplification of the CC present invention.
                                                                                                                                                                                               Query Match
Best Local s
Matches 848
                                                                                                                                                                                                                                                                            present invention.

N.B. Pages 666 to 682 and page 7053 of the missing at time of publication, meaning no SEQ ID NO:1027 to 1052, 7921 and 7922.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim
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03-NOV-1999;
                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acids encoding 4277 human useful for preventing, diagnosing
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                                                                               TCCGCGCGGCTGCTGCGAGCGGTGATCATGGGGGCCCCGGGCTCGGGCAAGGGCACCGTG
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GACAACATGCTGCGGGGCACAGAAATTGGCGTGTTAGCCAAGGCTTTCATTGACCAAGGG
                                         TCGTCGCGCATCACTACACACTTCGAGCTGAAGCACCTCTCCAGCGGGGACCTGCTCCGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                carcinoma;
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99US-0163280
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                                                                                                                                                                                               0;
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Pred. No. 4.5e-236;
0; Mismatches 6;
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                                                                                                                                                                                               CTGGNATATTACCAGAAAAAAGGGGTGCTGGAAACATTCTCCGGGAACAGAAACCAACAAG
                                                                                                                                                                                                                                CCTCCCAAAACTGTGGGGCATTGATGACCTGACTGGGGAGCCTCTCATTCAGCGTGAGGAT
                                                                                                                                                                                                                                                                                                                                        CGCCTTACTGCTCGCTGGATTCATCCCGCCAGTGGCCGAGTCTATAACATTGAATTCAAC
                       ATTATATTACTTTTA
                                                                                                                                        ATTTGGCCCTATGTATATGCTTTCCTACAAACTAAAGTTCCACAAAGAAGCCAGAAAGCT
                                                                                                                                                   ATTTGGCCCTATGTATATGCTTTCCTACAAACTAAAGTTCCACAAAGAAGCCAGAAAGCT
                                                                                                                                                                                                                                                        CCTCCCAAAACTGTGGGCATTGATGACCTGACTGGGGAGCCTCTCATTCAGCGTGAGGAT
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Human 11-JAN-2002 ABA09570; ABA09570 standard; secreted (first entry) CDNA; 2041 ВP

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protein homologue-encoding cDNA, SEQ ID NO:1346

RESULT 6
ABA09570
ID ABA09570
XX ABA0
AC ABA0
XX Huma
XX Huma
XX Huma
KW Huma
KW Inhi
KW Inhi bone disorder; osteoporosis; vascular growth disorder; tissue regeneration; wound healing; infection; immune disorder; cell culture; drug screening; gene therapy; antiinflammatory; antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic; myeloid cell disorder; lymphoid cell disorder; asthma; arthritis; chronic inflammatory condition; proliferative retinopathy; atherosclerosis; coronary heart disease; arterial ischaemia; Human; cytokine; cell proliferation; cell differentiation; growth f haematopoiesis regulation; tissue growth; immunomodulator; activin; inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis; proliferation; metastasis; cancer; tumour; haematopoietic disorder; cytostatic; antifungal; osteopathic; vasotropic; cardiant; virucide; antibacterial; factor;

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                                                                                                                                                                                                                                                                         Conditions, e.g., by protein or gene therapy. Such conditions include conditions, he manusomodulatory activity; activities; haemostatic, thrombotic or thrombolytic activities; receptor or ligand activities; or may be conditions, e.g., by protein or gene therapy. Such conditions include cancers, haematopoletic disorders (e.g., myeloid or lymphoid cell conditions, e.g., by protein or gene therapy. Such conditions include cancers, haematopoletic disorders (e.g., myeloid or lymphoid cell conditions, e.g., by protein or gene therapy. Such conditions include cancers, haematopoletic disorders (e.g., myeloid or lymphoid cell conditions, e.g., by protein or gene therapy. Such conditions include cancers, haematopoletic disorders (e.g., myeloid or lymphoid cell conditions, e.g., by protein or gene therapy. Such conditions include cancers, haematopoletic disorders (e.g., myeloid or lymphoid cell conditions, e.g., by protein or gene therapy. Such conditions include cancers, haematopoletic disorders (e.g., myeloid or lymphoid cell conditions, horeast (e.g., myeloid or lymphoid cell cancers, healthy to protein or gene therapy. Such conditions include cancers, healthy terminates (e.g., sethman or arthritis), coronary heart disease.

Conditions, e.g., by protein or gene therapy. Such conditions and abnormal conditions, and abnormal conditions and ulcers), while those with the above the factor activity may be used to promote wound the activity may be used in cell cultures to promote cell growth. For example, such polypeptides may be used to conditions, and incleotides and conditions and ulcers of the above conditions, and in drug screening techniques. The present sequence represents a cDNA encoding a covel human polypeptide of the invention.
                                                                                                                                                                                                 Query Match
                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or polypeptides in a sample, and methods of identifying compounds which bind to polypeptides of the invention. Although novel, many of the polypeptides of the invention have homology to known proteins, thereby giving an insight into their probable biological activities, and hence potential therapeutic applications. The polypeptides of the invention may have various activities, including cytokine, cell proliferation or cell differentiation activities; stem cell growth factor activity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and sequences ABA0825-ABA09574 represent nucleic acids encoding them. The invention also relates to vectors and recombinant host cells comprising a nucleotide of the invention, methods of producing the novel polypeptides, antibodies against the polypeptides, methods of detecting the nucleotides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 1007-1008; 1963pp; English.
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27-APR-2000;
                                                                                                                                                                                                                                            Sequence
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                                                                                      GGGCCTCAGTCTGCGGCCATGGGGGCGTCCGCCGCCGCTGCTGCGAGCGGTGATCATGGGG
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820;
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                                                                                                                                                                               Similarity
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2000US-0560875.
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Pred. No. 1.2e-231;
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                                                                                          Human: nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
                                                                                  chemokinetic; thrombolytic;
                                                                                                                                                      Human polynucleotide SEQ ID
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                                                                                                                                                                                                                         AAI59841 standard;
                                                                     leukaemia; ss
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WO200153312-A1 Homo sapiens.

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25-APR-2000;
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19-JUL-2000;
03-AUG-2000;
14-SEP-2000;
19-OCT-2000;
29-NOV-2000;
                                                                                                                                                                                                                                                                                                                            The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polypnucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, activinyinhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and
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Note: The sequence
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2000US-0552317.
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                                                                                                                                                                                                                                 Human; nootropic; immunosuppressant; cytostatic; gene therapy; c
peripheral nervous system; neuropathy; central nervous system; C
Alzheimer's; Parkinson's disease; Huntington's disease; haemosta
amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
chemokinetic; thrombolytic; drug screening; arthritis; inflammat
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Tang Wang 2hao

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Liu C, Wang Z, Zhou P,

Asundi V, Wehrman T, Goodrich R

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Best Local Similarity
Matches 818; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM8642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activity semotactic/chemokinetic activity, hemostatic and thrombolytic activity, chemotactic/chemokinetic activity, hemostatic assays for receptor activity, arthritis and inflammation, leukaemias and
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                                                                                                              GGGGAGCCTCTCATTCAGCGTGAGGATGATAAACCAGAGACGGTTATCAAGAGACTAAAG
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                              GCTTATGAAGACCAAACAAAGCCAGTCCTGGAATATTACCAGAAAAAAGGGGTGCTGGAA
                                          GCTTATGAAGACCAAACAAAGNCAGTCCTGGNATATTACCAGAAAAAAAGGGGTGCTGGAA
                                                                        GGGGAGCCTCTCATTCAGCGTGAGGATGATAAACCAGAGACGGTTATCAAGAGACTAAAG
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)B; AAM38899.
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The present invention describes primer sets for synthesising 5602 (C full-length cDNAs defined in the specification. Where a primer set (C comprises: (a) an oligo-dT primer and an oligonucleotide complementary (CC to the complementary strand of a polynucleotide which comprises one of (CC the 5602 nucleotide sequences defined in the specification, where the (CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination (CC of an oligonucleotide comprising a sequence complementary to the (CC complementary strand of a polynucleotide which comprises a 5'-end (CC complementary strand of a polynucleotide which comprises a 5'-end (CC complementary to a complementary for comprises a 3'-end sequence (where the comprises a 3'-end sequence, where the (CC cligonucleotide comprises a 1'-end sequence, where the (CC clig
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                                                                                                                                                                                                                                                                                                                                                                                                     Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-JUL-1999; 99JP-0248036.
27-AUG-1999; 99JP-0300253.
11-JAN-2000; 2000JP-0118776.
02-MAY-2000; 2000JP-0183767.
09-JUN-2000; 2000JP-0241899.
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represent oligonucleotides,
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                                                                                                                                                                                                                                                                                                                                  The invention relates to a cDNA (clone C-NT2RP2000329) encoding a novel adenylate kinase 3 (AK3)-like protein. C-NT2RP2000329 has functions of converting extracellular signals into intracellular signals and changing cell morphology. The AK3-like protein, polynucleotides and antibodies are useful in the investigation of diseases such as MELAS (cerebral accident condition with hyperlacticacidemia), central nervous system disorder, epilepsy, skeletal muscle conditions, muscle disease, electron transfer disorders, Leber disease, diabetes mellitus, Peason disease, Parkinson's disease, metabolism disorders. They are useful for developing diagnostics and treatment agents. The present sequence represents a cDNA encoding a human AK3-like protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27-AUG-1999;
18-OCT-1999;
11-JAN-2000;
17-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New gene encoding an adenylate kinase 3-like protein, and the and antibodies to it, useful for diagnosis of brain disease epilepsy, muscle disease, genetic disorder, diabetes -
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                                                                                                                                                                                                                                                                                                   Sequence
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Sugiyama T, Wakamatsu A,
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                                                                                                                                          CTCAGTCTGCGGCCATGGGGGGCGTCCGCGCGCGCTGCTGCGAGCGGTGATCATGGGGGCCCC
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                                                                                                                                                                                                                       al Similarity 99.8
816; Conservative
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2000US-0183322.
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Nagai K,
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                                                                                                      28-SEP-1998;
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P-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 751 BP; 211 A; 189 C; 186 G; 165 T; 0 other;
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                                 GCCCTAGATAGAGCTTATCAGATCGACACAGTGATTAACCTGAATGTGCCCTTTGAGGTC
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DB; AAB12440.
          AAACCTCCTAGTCCTTGCATTTAGAAGCTGC 801
                                                                                                                                            CGTGAGGATGATAAACCAGAGACGGTTATCAAGAGACTAAAGGCTTATGAAGACCAAACA
                                                                                                                                                                                                                   AATCTCACCCAGTATAGCTGGCTGTTGGATGGTTTTCCAAGGACACTTCCACAGGCAGAA
                                                                                                                                                                                                                                     ATTAAACAACGCCTTACTGCTCGCTGGATTCATCCCGCCAGTGGCCGAGTCTATAACATT
                                                                                                                                                                                                                                                      GCCCTAGATAGAGCTTATCAGATCGACACAGTGATTAACCTGAATGTGCCCCTTTGAGGTC
                                                                                                                                                                                                                                                                                         AATCTCACCCAGTATAGCTGGCTGTTGGATGGTTTTCCAAGGACACTTCCACAGGCAGAA
AAACCTCCTAGTCCTTGCATTTAGAAGCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              85.5%;
98.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 729.8;
Pred. No. 3.
751
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                                                                                                                                                                                                                                  CC AAC97991 to AAC98763 encode the human colon cancer associated proteins, CC called human colon cancer antigens, given in AAB53234 to AAB54006. The CC human colon cancer antigens can have cytostatic, cardioactive, muscular; CC entroprotective, immunomodulatory, gynaecological, gastrointestinal, CC vulnerary, nephrotropic, antiinfective and antibacterial activities, and CC can be used in gene therapy. The colon cancer antigen polynucleotides, CC proteins and antibacies to the proteins are useful for the prevention, CC treatment and diagnosis of colon disorders, such as colon cancer. The CC polynucleotides may be used in diagnostics and research, such as for CC chromosome identification, and as hybridisation probes. The proteins CC may also be used to prevent diseases such as neural disorders, immune CC system disorders, muscular disorders, reproductive disorders, such as proteins CC gastrointestinal disorders, wounds, renal disorders, infectious CC diseases, and cardiovascular disorders. AAC98764 to AAC98772 and AAB54007 represent sequences used in the exemplification of the present
                                                                                                                                                    Matches
                                                                                                                                                                Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Colon cancer associated gene sequences, referred antigens, useful for the treatment, prevention, a disorders such as colon cancer -
                                                                                                                                                                                                    Sequence 733
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 849; 2104pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-MAR-2000; 2000WO-US05883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nephrotropic; antiinfective; antibacterial; gene therapy; wound; neural disorder; immune system disorder; muscular disorder; reproductive disorder; gestrointestinal disorder; renal disorder; infectious disease; cardiovascular disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200055351-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; colon cancer; colon cancer antigen; diagnosis; detection; identification; cytostatic; cardioactive; neuroprotective; vulne immunomodulatory; muscular; gynaecological; gastrointestinal; nephrotropic; antiinfective; antibacterial; gene therapy; wound;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAC98376 standard; cDNA; 733
                    198
                                            61
                                                                                                        78 GCGGTGATCATGGGGGCCCCGGGCTCGGGCAAGGGCAACCGTGTCGTCGCGCATCACTACA 137
                                       CACTTCGAGCTGAAGCACCTCTCCAGCGGGGACCTGCTCCGGGACAACATGCTGCGGGGC
 ACAGAAATTGGCGTGTTAGCCAAGGCTTTCATTGACCAAGGGAAACTCATCCCAGATGAT
                                                                                         GCGGTGATCATGGGGGCCCCGGGCTCGGGCAAGGGCACCGTGTCGTCGCGCATCACTACA
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DB; AAB53619.
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                                                                                                                                                             Similarity
                                                                                                                                                    Conservative
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                                                                                                                                                                                                      213
                                                                                                                                                             81.0%;
97.5%;
                                                                                                                                                                                                    A; 175
                                                                                                                                                                                                   C; 173 G; 168 T; 4 other;
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                                                                                                                                               Score 691.4; DB Pred. No. 7e-194; O; Mismatches ]
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                                                                                                                                                 17;
                                                                                                                                                                       21; Length
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Ota T, 1
Ishii S,
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11-JAN-2000;
02-MAY-2000;
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                                                                                                                                             07-FEB-2001
                                                                                                                                                                                                             Human;
                                  (HELI-)
                                                                                                   29-JUL-1999;
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                                                                                                                                                                                                                                   CDNA
                                                                                                                                                                                                            primer;
 Isogai T,
, Sugiyama
                                  HELIX RES INST.
                                                                                                                                                                                                                                  clone
                                                      99JP-0300253.
2000JP-0118776.
2000JP-0183767.
2000JP-0241899.
                                                                                                                                                                                                                                                                                                                                                                           804
                                                                                                                         2000EP-0116126
                                                                                                                                                                                                                                                       (first entry)
                                                                                                   99JP-0248036
                                                                                                                                                                                                             detection; diagnosis;
                                                                                                                                                                                                                                 (5'-primer) SEQ ID
            Nishikawa T,
Hayashi K,
A, Nagai K
                                                                                                                                                                                                                                   NO:3211.
                                                                                                                                                                                                            antisense therapy;
 Saito K,
Otsuki
  Yamamoto
T;
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Wakamatsu

Nagai K,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             comprises: (a) an oligo-dr primer and an oligonucleotide comprises one of the 5602 nucleotide sequences defined in the specification, where the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the coligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprises as sequence complementary to the complementary strand of a polynucleotide which comprises a 5 end complementary to a complementary for comprises at least 15 nucleotides and the combination of the 5 end sequence/3' end sequence is selected from those defined in the specification. The primers set useful for synthesising polynucleotides, and comparison to be useful for the particularly full-length cDNAs. The primers are useful for synthesising polynucleotides, comparison to the specification and complementary of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH33166 to AAH33628 and CDNAH3333 to AAH318742 represent human cDNA sequences; AAB92446 to compresent oligonucleotides, all of which are used in the exemplification confidence of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Ma
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs -
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                                                                                        AAACTCATCCCAGATGATGTCATGACTCGGCTGGCCCTTCATGAGCTGAAAAATCTCACC
                                                                                                                                                                                                                                                                                                   GACAACATGCTGCGGGGCACAGAAATTGGCGTGTTAGCCAAGGCTTTCATTGACCAAGGG
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CCTCCCAAAACTGTGGGCATTGATGACCTGACTGGGGAGCCTCTCATTCAGCGTGAGGAT
                                               CGCCTTACTGCTCGCTGGATTCATCCCGCCAGTGGCCGAGTCTATAACATTGAATTCAAC
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                                                                                                                                                                                                                      AAACTCATCCCAGATGATGTCATGACTCGGCTGGCCCTTCATGAGCTGAAAAATCTCACC
                                                                                                                                                                                                                                                                                  GACAACATGCTGCGGGGCACAGAAATTGGCGTGTTAGCCAAGGCTTTCATTGACCAAGGG
                                                                                                                                                                                                                                                                                                                                                 TCGTCGCGCATCACTACACACTTCGAGCTGAAGCACCTCTCCAGCGGGGACCTGCTCCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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94.8%;
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Pred. No. 2.5e
0; Mismatches
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RESULT 14
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27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
                       of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to polynucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination the 5'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and the specification.
                                                                                                                                                                                                The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination
                                                                                                                                                                                                                                                                                                                                                                                                                              Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ishii
                                                                                                                                                                                                                                                                                                                                                                                    Claim
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, Sugiyama
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99JP-0300253.
2000JP-0118776.
2000JP-0183767.
2000JP-0241899.
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T, Wakamatsu
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A, Nagai K,
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, Otsuki
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Best Local S
Matches 614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAB95893 represent oligonucleotides, all of which are used in the exemplification of the present invention.
  Homo
                                                           26-JUN-2001
                                                                               AAH07675;
                                                                                                   AAH07675 standard;
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                                                                                                                                                                                                                                                                               GAGTCTATAACATTGAATTCAACCCTCCCAAAACTGTGGGCATTGATGACCTGACTGGGG
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                                                                                                                                                   TCTCCGGAACANAAACCAACAANATTTGGNCCTATTTTT
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                                                                                                                                                                     TCTCCGGAACAGAAACCAACAAGATTTGGCCCTATGTAT
                                                                                                                                                                                        ATGAAGACCAAACCAAACCAGTCCTGGAAATATTACCANAAAAAANGGGTGCTGGAAACAT
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                                        CDNA
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614; Conservative
                    primer;
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                   detection;
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                    diagnosis;
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Pred. No. 1.8e
0; Mismatches
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                   antisense therapy;
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.8e-165;
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                   gene therapy;
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GACAACATGCTGCGGGGCACAGAAATTGGCGTGTTAGCCAAGGCTTTCATTGACCAAGGG

TCGTCGCGCATCACTACACACTTCGAGCTGAAGCACCTCTCCAGCGGGGACCTGCTCCGG

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TCCGCGCGGCTGCTGCGAGCGGTGATCATGGGGGCCCCGGGCCTCGGGCAAGGGCACCGTG GGCCAGGCCAAAGCCCTGGTACCCGCGCGCGGTGCGGGCCTCAGTCTGCGGCCCATGGGGGGCG

TCCGCGCGCTGCTGCGAGCGGTGATCATGGGGGCCCCGGGCTCGGGCAAGGGCACCGTG

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CC full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dy primer and an oligonucleotide complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprises as sequence complementary strand of a polynucleotide which comprises a 5'-end CC polynucleotide which comprises a 3'-end sequence complementary to a complementary complementary to a complementary 
                     Query Match
Best Local
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11-JAN-2000;
02-MAY-2000;
09-JUN-2000;
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                                                                                  Sequence
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Local Similarity es 617; Conserv
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, Sugiyama
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67.8%;
nilarity 97.6%;
Conservative
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T, Wakamatsu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2537pp + CD ROM;
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Score 578.6;
Pred. No. 1.6e
0; Mismatches
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A, Nagai K
                                                                                ç;
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                       .6e-160;
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                                          DB 22;
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                                                                                  other;
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	Db 662 TCCTGGGATATTACCAAGAAAAAAGGGGGTG 693
	Qy 598 TCCTGGNATATTACCAGAAAAAAGGGGTGCTG 629
661	Db 602 TTGATAAACCAGAGACGGTTATCAAGAGACTAAAGGCTTATGAAGACCAAACAAA
597	- 41
601	Db 542 CCTCCCAAAACTGTGGGCATTGATGACCTGACTGGGGAGCCTCTCATTCAAGCGTGAGGA
538	
541	Db 482 CGCCTTACTGCTCGCTGGATTCATCCCGCCAGTGGCCGAGTCTATAACATTGAATTCAAC
479	- 12
481	Db 422 AGAGCTTATCAGATCGACACAGTGATTAACCTGAATGTGCCCTTTGAGGTCATTAAACAA
419	
421	Db 362 CAGTATAGCTGGCTGTTGGATGGTTTTCCAAGGACACTTCCACAGGCAGAAGCCCTAGAT
359	3
361	Db 302 AAACTCATCCCAGATGATGATGACTCAGGCTGGCCCTTCATGAGCTGAAAAATCTCACC

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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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                                                                                                                                                                 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
       832.6
797.4
699.2
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Match
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## ALIGNMENTS

FEATURES Source		TITLE JOURNAL COMMENT	REFERENCE AUTHORS	ACCESSION VERSION KEYWORDS SOURCE ORGANISM	RESULT 1 BM923355 LOCUS DEFINITION
http://lmage.lini.gov Plate: LLAM12803 row: j column: 14 High quality sequence stop: 686. Location/Qualifiers 11070	Email: cgapbs-remail.nih.gov Tissue Procurement: Life Technologies, Inc. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:	National Institutes of Health, Mammallan Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo.  1 (bases 1 to 1070)  NIH-MGC http://mgc.nci.nih.gov/.	BM923355 BM923355.1 GI:19373734 EST. human. Homo sapiens	BM923355 AGENCOURT_6625937 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5758957 5', mRNA sequence.

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BASE COUNT
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                                                                                                             CTGGNATATTACCAGAAAAAAGGGGTGCTGGAAACATTCTCCGGGAACAGAAACCAACAAG
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                                  CCTCCCAAAACTGTGGGCATTGATGACCTGACTGGGGAGCCTCTCATTCAGCGTGAGGAT
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/db_xref="taxon:9606"
/clone="IMAGE:5758957"
/clone=11b="NIH_MGC_116"
/lab_host="DH10B"
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Pred. No. 8.4e-226;
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TCGTCGCGCATCACTACACACTTCGAGCTGAAGCACCTCTCCAGCGGGGACCTGCTCCGG
                                                                         TCCGCGCGGCTGCTGCGAGCGGTGATCATGGGGGCCCCGGGCTCGGGCAAGGGCACCGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CGAP (Stanford)
CDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 979)

NIH-MGC http://mgc.nci.nih.gov/.
mational Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                        /clone_lib="NH_MCC_100"
/clone_lib="NH_MCC_100"
/tissue_type="hepatocellular carcinoma, cell line"
/lab_host="PH10B (phage=resistant)"
/lab_host="PH10B (phage=resistant)"
/note="Organ: liver; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor:
GCCACCAG(G). Size=selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
IRT (Life Technologies). Note: this is a NIH_MGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:9606"
/clone="IMAGE:6284963"
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AGENCOURT_7050937 NIH_MGC_71 H
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BQ050240
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                                           Contact: Robert Strausberg, | Email: cgapbs-r@mail.nih.gov Tissue Procurement: ATCC
                                                                           NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
                                                                                                          Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1024)
                                                                                                                                                       human
CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can
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Plate: LLAM12869 row: c
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/db_xref="taxon:9606"
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/clone_lb="NHH_MGC_71"
/tissue_type="leiomyosarcoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: uterus; vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 2.1 kb. "
a 251 c 240 g 231 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shira
Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11694 row: b column: 05
High quality sequence stop: 763.
Location/Qualifiers
GCCANGCCCAAAGCCCTGGTACCCGCGCGGTG-GGGCCTCAGTCTGCGGCCATGGGGGGCG
                                                         TCGTCGCGCATCACTACACACTTCGAGCTGAAGCACCTCTCCCAGCGGGGACCTGCTCCGG
                                                                                                      TCCGCGCGGCTGCGAGCGGTGATCATGGGGGCCCCGGGCTCGGGCAAGGGCACCGTG
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                                              TCGTCGCGCATCACTACACACTTCGAGCTGAAGCACCTCTCCAGCGGGGACCTGCTCCGG
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection Unpublished (1999)
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                                                                                          Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI), Sh
Toshiyuki and Piero Carninci (RIKN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleosto Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 706)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                found through the I.M.A.G.E. Consortium/LLNL http://image.llnl.gov plate: LLMH00725 row: g column: 08 High quality sequence stop: 706.
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602687928F1 NIH_MGC_95
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CCTCCCAAAACTGTGGGCATTGATGACCTGACTGGGGAGCCTCTCATTCAGCGTGAGGAT
                                                AGAGCTTATCAGATCGACACAGTGATTAACCTGAATGTGCCCTTTGAGGTCATTAAACAA 419
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Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HRI human cDNA project Unpublished (2000)
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Ota,T., Nishikawa,T.,
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/cell_line="NTO"
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/db_xref="taxon:9606"
/clone="NT2RP3000359"
/clone_lib="NT2RP3"
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                                                                                                                      CGCATCACTACACACTTCGAGCTGAAGCACCTCTCCAGCGGGGACCTGCTCCGGGACAAC
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                                                                                                          CGCATCACTACACACTTCGAGCTGAAGCACCTCTCCAGCGGGGACCTGCTCCGGGACAAC
                    ATCCCAGATGATGTCATGACTCGGCTGGCCCTTCATGAGCTGAAAAATCTCACCCAGTAT
                                                ATGCTGCGGGGCACAGAAATTGGCGTGTTAGCCCAAGGCTTTCATTGACCAAGGGAAACTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Zeguang Han
Chinese National Human Genor
351 Guo Shoujing Road, Zhang
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
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,H., Xu,X., Li,N., Qian,B.,
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1 (bases 1 to 716)
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xu,X., L1,N., Qian,B., Liu,F., Qu,J., Gao,X., Cheng,Z., Xu,
L1., Xu,S., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M., L
Hu,R., Chen,J., Chen,Z. and Han,Z.
sapiens CDNA ADB clones
                                                                                                                                                                                                                                                                                                                                                                                                                              clone
                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                             hanzg@chgc.sh.cn
lone is available at CHGC
Location/Qualifiers
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XhoI"
                                                                                                                                                                                                                                                                                         /tissue_type="Adrenal gland"
/dev_stage="Adult"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="ADBBXH03"
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/clone_lib="ADB"
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BG106150
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                                                                                                                                                                 Tissue Procurement: Louis Staudt, M.D., Ph.D. CDNA Library Preparation: Life Technologies, Inc. CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                          1 (bases 1 to 1183)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
                                                                                                                                    found through the I.M.A.G.E. Consortium/LLNL http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/organism "Homo sapiens"
/db_xref = "taxon:9606"
/clone="IMAGE:4385034"
/clone_lib="NIH_MGC_85"
/tissue_type="lymphoma, c
                                                                                         Location/Qualifiers
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   cell line"
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                                     BQ435142
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AGENCOURT_7914060 NIH_MGC_71
5', mRNA sequence.
Homo sapiens
Eukaryota; M
                  human.
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/note="Organ: lymph; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.867 kb. Library enriched for
full-length clones and constructed by Life Technologies
Note: this is a NIH_MGC Library."
273 c 334 g 231 t
Metazoa;
                                      GI:21174218
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Chordata;
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Pred. No. 1.2e-169;
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Craniata;
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Query Match
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                                                                                                                                                                                                                                                                                                                                  TGATGACCTGACTGGGGAGCCTCTCATTCAGCGTGAGGATGATAAACCAGAGACGGTTAT 559
                                                                                                                                                                                                                                                                                                                                                                                                                   TCATCCCGCCAGTGGCCGAGTCTATAACATTGAATTCAACCCTCCCAAAACTGTGGGCAT 499
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                                                                                                                                            CAAGAGACTAAAGGCTTATGAAGACCAAACAAGCCAGTCCTGGAATATTACCAGAAAAA
                                                                                                                                                                                                                                                 CAAGAGACTAAAGGCTTATGAAGACCAAACAAAGNCAGTCCTGGNATATTACCAGAAAAA 619
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NIH-MGC http://mgc.nci.nih.gov/.
NATIONAL INSTITUTES of Health, M
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Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph
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/db_xref="taxon:9606"
/dlone="IMAGE:6156916"
/clone="IMAGE:6156916"
/clone_lib="NIH_MCC_71"
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/lab_host="Organ: uterus; Vector: pcMV-SPORT6; Site_1: Not Site_2: Sali; Cloned unidirectionally. Primer: Oligo Average insert size 2.1 kb. "
10 a 191 c 213 g 239 t 1 others
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97.9%;
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Pred. No. 3.
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3.1e-169;
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                                         TCCGCGCGGCTGCCGAGCGGTGATCATGGGGGCCCCGGGCTCGGGCAAGGGCACCGTG
               GACAACATGCTGCGGGGCACAGAAATTGGCGTGTTAGCCAAGGCTTTCATTGACCAAGGG
                                                                    TCGTCGCGCATCACTACACACTTCGAGCTGAAGCACCTCTCCAGCGGGGACCTGCTCCGG
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Email: Cgapbs r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MCC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L/LAM11660 row: J column: 19
High quality sequence stop: 801.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 833)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collections (1988)
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603190877F1 NIH_MGC_95 Homo:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1999)
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/db_xref="taxon:9606"
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/clone_lib="NIH_MGC_95"
                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="hippocampus"
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                                                                                                                                                                                                                  73.3%;
                                                                                                                                                                                                                  Score 625.8; DB 13; Pred. No. 5.6e-167;
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                                                                                                                                                                                    Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                              http://image.llnl.gov
Plate: LLCM1590 row: p column:
High quality sequence stop: 772.
Location/Qualifiers
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602618148F1 NIH_MGC_79 Homo
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TCCTGGNATATTACCAG-AAAAAAGGGGTGCTGGAAACATTCTCCGGAACAAAACCAAC
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                                                                              CCTCCCAAAACTGTGGGCATTGATGACCTGACTGGGGAGCCTCTCATTCAGCGTGAGGAT
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 902)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)

Contact: Robert Strausberg, Ph.D. 902 bp 2 bp mRNA linear EST 18-APR-2001 sapiens cDNA clone IMAGE:4731898 5',

/organism="Homo sapiens" /db\_xref="taxon:9606" /clone="IMAGE:4731898"

11

be

/Clone="IMMOC\_79"
/Clone\_Tib="NIH\_MCC\_79"
/lab\_host="DH10B (T1 phage-resistant)"
/note="organ: placenta; Vector: pDNR-LIB (Clontech);
/note="organ: placenta; Vector: pDNR-LIB (Clontech);
// Site\_1: SfiI (ggccgctcggcc); Site\_2: SfiI (ggccattatggcc); Site\_2: SfiI (ggccattatggcc); Site\_2: Add 3' adaptors were used in cloning as follows: 5'); S' and 3' adaptors were used in cloning as follows: 5'); S' and 3' adaptors were used in cloning as follows: 5'.

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ACCESSION
VERSION
KEYWORDS
                                                                                                                 RESULT 12
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Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 639)
Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K.,
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                                                                                              NT2RP2
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 TCTCCGGAACAGAACCAACAAGATTTGGCCCTATGTAT
                   ATGAAGACCAAACCAAACCAGTCCTGGAAATATTACCANAAAAAANGGGTGCTGGAAACAT
                                     ATGAAGACCAAACAAAGNCAGTCCTGGNATATTACCAGAAAAAAGGGGGTGCTGGAAACAT
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HRI human cDNA
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/ Match 69.7%;
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nes 614; Conservative
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                  CGGGCTCGGGCAAGGGCACCGTGTCGTCGCGCATCACTACACACTTCGAGCTGAAGCACC
CGGGCTCGGGCAAGGGCACCGTGTCGTCGCGCATCACTACACACTTCGAGCTGAAGCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
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1532-3 Yana, Kisarazu, Chiba
Tel: 81-438-52-3975
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Contact: Takao Isogai
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                                                                                                                                                                                                                                                                                                                                    /db_xref="Homo sapiens"
/db_xref="taxon:9606"
/clone="NT2RP2000329"
/clone_lib="NT2RP2"
/cell_type="teratocarcinoma"
/cell_line="NT2"
                                                                                                                                                                                                                                                                                      /note-"Vector: pME18SFL3; mRNA from NT2 neuronal cells after 2-weeks retinoic acid (RA) induction 167 c 155 g 138 t 9 others
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Pred. No. 2.6e-158;
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                                                                            AAACTCATCCCAGATGATGTCATGACTCGGCTGGCCCTTCATGAGAGAAAATCTCACC
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CAGTATAGCTGGCTGTTGGATGGTTTTCCAAGGACACTTCCACAGGCAGAAGCCCTAGAT
                                      AAACTCATCCCAGATGATGTCATGACTCGGCTGGCCCTTCATGAGCTGAAAAATCTCACC
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Insight into hepatocellular carcinogenesis at transcriptome level by comparing gene expression profiles of hepatocellular carcinoma with those of corresponding noncancerous liver Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
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AV695155
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Chinese National Human
351 Guo Shoujing Road,
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86-21-50801919(ex.45)
86-21-50801922
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clone is available at CHGC
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/dev_stage="Adult"
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/db_xref="taxon:9606"
/clone="GKCASD12"
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Zhangjiang Hi-Tech Park,
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Plate: LLCM1616 row: h column:
                                                                                                                                                                                                                                                                                                                                                                                                   Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D.
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                          cDNA Library Preparation: CLONETECH Laboratories, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     625;
                       nki numan cDNA project
Unpublished (2000)
Contact: Takao Isogai
Genomics Laboratory
Heliv paggarant
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AU136907.1
EST.
                                                                                                                                          AU136907
AU136907
                                                            Ota,T., Nishikawa,T., Suzul
Yamamoto,J., Wakamatsu,A.,
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba
Tel: 81-438-52-3975
Fax: 81-438-52-3986
                                               Isogai,T.
HRI human cDNA
                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
1 (bases 1 to 803)
                                                                                         Homo sapiens
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Primates;
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Pred. No. 3e-154;
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                                                            Nakamura,Y., Na
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Matches 617;
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                                                      CCTCCCAAAACTGTGGGCATTGATGACCTGACTGGGGAGCCTCTCATTC-AGCGTGAGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: He.
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo,
Helix Research Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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/tissue_type="placenta"
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                                                                                                                                                                                                                                                                                                                                                                                                           /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
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US-07-626-618A-1

US-07-928-611-1

US-08-333-977-1

US-08-487-811A-1

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US-09-378-074-1

PCT-US93-07370-1

US-08-758-662-4
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Query Match 99.6%; Score 851; DB 2; L Best Local Similarity 100.0%; Pred. No. 2.3e-248; Matches 854; Conservative 0; Mismatches 0;
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MEDIUM TYPE: Diskett
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                                            MEDIAL COUSTINE: 2122022
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OPERATING SYSTEM:
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CITY: Palo Alto
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	ppl	Appli	App1	Appl	Appl	Appl	Appl	App11	Appi	Appi	Appl	Appl	Appl	App1:	Appl	Appl	Appl

## ALIGNMENTS

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Sequence 2, Application US/08829027
Patent NO. 5856160
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Shah, Purvi
TITLE OF INVENTION: NOVEL MITOCHO
NUMBER OF SEQUENCES: 5
               INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 854 base pairs
TYPE: nucleic acid
                                                                                                                                      FILIG DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Billings, Lucy J.

REGISTRATION NUMBER: 36,749

REFERENCE/DOCKET NUMBER: PF-0

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/829 077
FILING DATE:
                                                                                                                                                                                                                                                                                                                FILING DATE: Herewith CLASSIFICATION: 435 PRIOR APPLICATION DATA:
STRANDEDNESS: single
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                                                       Sequence 2, Application Patent No. 6001624
GENERAL INFORMATION:
        APPLICANT: Hilman, Jennifer L.
APPLICANT: Shah, Purvi
TITLE OF INVENTION: NOVEL MITOCHONDRIAL
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
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APPLICATION NUMBER: US/09/225,36
FILING DATE:
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION UMBER: 08/829,027
FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
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LENGTH: 854 base pairs
TYPE: nucleic acid
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MEDIUM TYPE: Diskett
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US-09-149-476-68 US-09-149-476-68 Sequence 68, Application US/09149476 Sequence 69, Application US/09149476 GENERAL INFORMATION: 186 Human Secreted proteins FILE REFERENCE: P2002p1 FILE REFERENCE: P2002p1 CURRENT APPLICATION NUMBER: US/09/149,476 CURRENT APPLICATION NUMBER: US/09/149,476 CURRENT PILING DATE: 1989-03-06 EARLIER APPLICATION NUMBER: 60/040,162 EARLIER APPLICATION NUMBER: 60/040,33 EARLIER FILING DATE: 1999-03-07 EARLIER APPLICATION NUMBER: 60/040,33 EARLIER FILING DATE: 1999-03-07 EARLIER APPLICATION NUMBER: 60/040,33 EARLIER FILING DATE: 1999-03-07 EARLIER FILING DATE: 1997-03-07 EARLIER APPLICATION NUMBER: 60/040,33 EARLIER FILING DATE: 1997-03-07 EARLIER FILING DATE: 1997-03-0	Db 481 CTCCCAAAACTGTGGGCATTGATGACTGACTGGGAAGCCTCTCATTCAGCAGAAGACGATGAGACTGAAACCAAACAAA
EARLIER FILING DATE: 1997-04-11 EARLIER APPLICATION NUMBER: 60/043,568 EARLIER APPLICATION NUMBER: 60/043,314 EARLIER FILING DATE: 1997-04-11 EARLIER FILING DATE: 1997-04-11 EARLIER APPLICATION NUMBER: 60/043,311 EARLIER FILING DATE: 1997-04-11 EARLIER FILING DATE: 1997-04-11 EARLIER FILING DATE: 1997-04-11 EARLIER FILING DATE: 1997-04-11 EARLIER APPLICATION NUMBER: 60/043,671 EARLIER APPLICATION NUMBER: 60/043,671 EARLIER APPLICATION NUMBER: 60/043,672 EARLIER FILING DATE: 1997-04-11 EARLIER FILING DATE: 1997-04-11 EARLIER FILING DATE: 1997-04-11 EARLIER FILING DATE: 1997-04-11 EARLIER APPLICATION NUMBER: 60/043,312 EARLIER FILING DATE: 1997-04-11 EARLIER APPLICATION NUMBER: 60/043,313 EARLIER FILING DATE: 1997-04-11 EARLIER FILING DATE: 1997-04-12 EARLIER APPLICATION NUMBER: 60/056,872 EARLIER APPLICATION NUMBER: 60/056,872 EARLIER APPLICATION NUMBER: 60/056,872 EARLIER APPLICATION NUMBER: 60/056,893 EARLIER FILING DATE: 1997-08-22 EARLIER APPLICATION NUMBER: 60/056,630 EA	REILING DATE: 1997-05- RAPPLICATION NUMBER: 6 REILING DATE: 1997-05- RAPPLICATION NUMBER: 6 REILING DATE: 1997-05- RAPPLICATION NUMBER: 6

R APPLICATION NUMBER: 60/030
R FILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/051
ER FILING DATE: 1997-08-22
ER APPLICATION NUMBER: 60/05
ER FILING DATE: 1997-08-22

60/056,888

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R FILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/05
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60/056,911 60/056,894

APPLICATION NUMBER: 60/ FILING DATE: 1997-08-22

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ER FILLING DATE: 1997-09-05
ER APPLICATION NUMBER: 60/056,884
ER FILLING DATE: 1997-08-22
ER APPLICATION NUMBER: 60/057,669
ER FILLING DATE: 1997-09-05
ER APPLICATION NUMBER: 60/049,610
ER FILLING DATE: 1997-06-13
ER FILLING DATE: 1997-06-13
ER FILLING DATE: 1997-06-13
ER FILLING DATE: 1997-10-02
                                              ATTTGGCCCTATGTATATGCTTTCCTACAAACTAAAGTTCCACAAAGAAGCCAGAAAGCT
                                                                                                                                                       CCTCCCAAAACTGTGGGCATTGATGACCTGACTGGGGAGCCTCTCATTCAGCGTGAGGAT
                                                                                                                                                                                                             TCCGCGCGGCTGCTGCGAGCGGTGATCATGGGGGCCCCGGGCTCGGGCAAGGGCACCGTG
              CTGGNATATTACCAGAAAAAAGGGGTGCTGGAAACATTCTCCGGGAACAGAAACCAACAAG
                                                                                                                                                                                                                                             CAGTATAGCTGGCTGTTGGATGGTTTTCCAAGGACACTTCCACAGGCAGAAGCCCTAGAT
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ATTATATTACTTTTA
                                                                                                                CTGGAATATTACCAGAAAAAAGGGGTGCTGGAAACATTCTCCGGAACAGAAACCAACAAG
                                                                                                                                               AAACTCATCCCAGATGATGTCATGACTCGGCTGGCCCTTCATGAGCTGAAAAATCTCACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97.8%;
99.2%;
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Pred. No. 2.1e
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2.1e-243;
nes 6;
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ER APPLICATION NUMBER: 60/05
ER FILING DATE: 1997-08-22
ER APPLICATION NUMBER: 60/06
ER FILING DATE: 1997-08-23

60/056,845

60/056,631

60/056,892

/057,761

60/047,595

ER APPLICATION NUMBER: 60/047,599
ER FILING DATE: 1997-05-23
ER APPLICATION NUMBER: 60/047,586
ER FILING DATE: 1997-05-23
ER APPLICATION NUMBER: 60/047,586
ER FILING DATE: 1997-05-23
ER APPLICATION NUMBER: 60/047,590
ER FILING DATE: 1997-05-23
ER APPLICATION NUMBER: 60/047,590
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ER FILING DATE: 1997-05-23
ER FILING DATE: 1997-05-23
ER APPLICATION NUMBER: 60/047,593
ER APPLICATION NUMBER: 60/047,593
ER APPLICATION NUMBER: 60/047,593
ER APPLICATION NUMBER: 60/047,614
ER FILING DATE: 1997-05-23
ER APPLICATION NUMBER: 60/047,578
ER APPLICATION NUMBER: 60/043,578
ER APPLICATION NUMBER: 60/043,670
ER FILING DATE: 1997-04-11
ER APPLICATION NUMBER: 60/043,670
ER APPLICATION NUMBER: 60/056,632
ER APPLICATION NUMBER: 60/056,664
ER APPLICATION NUMBER: 60/056,664
ER FILING DATE: 1997-08-22
ER APPLICATION NUMBER: 60/056,876
ER APPLICATION NUMBER: 60/056,876
ER APPLICATION NUMBER: 60/056,876
ER APPLICATION NUMBER: 60/056,876
ER APPLICATION NUMBER: 60/056,875
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ER APPLICATION NUMBER: 60/056,875
ER APPLICATION NUMBER: 60/056,862
ER APPLICATION NUMBER: 60/056,862
ER APPLICATION NUMBER: 60/056,875
ER APPLICATION NUMBER: 60/056,875
ER APPLICATION NUMBER: 60/056,862
ER APPLICATION NUMBER: 60/056,875
ER APPLICATION

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US-09-134-001C-452
; Sequence 452, Application US/09134001C
; Patent No. 6380370
RESULT 5
US-08-961-527-65
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APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NICLEIC ACID AMD AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR REILING DATE: 1997-11-08
PRIOR REPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER FILING DATE: 1997-08-14
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Best Local Similarity
Matches 286; Conserv
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SEQ ID NO 452
LENGTH: 669
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                                                                                                    607 ATTACCAGAAAAAAGGGGTGCTGGAAACATTCTCCGGAACAGAA 650
                                                                                                                                                                                                     395 CAGGTCGTCGTATCTGTGAGAAATGTGGTACAACATATCATCTTGTATTTAATCCTCCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     275 GATTCCCAAGAACTATAGATCAAGCTGAGTCATTAAATCAAATTATGTCTGAGCTTGATA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               265 CTCGGCTGGCCCTTCATGAGCT---GAAAAATCTCACCCAGTATAGCTGGCTGTTGGATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95 CAATACCACATATTTCTACTGGTGACATGTTCAGAAAAGCGATTAAAGATGAAACAGATT
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                                                                                                                                                                                                                                                                         AAACTGTGGGCATTGATGACCTGACTGGGGAGCCTCTCATTCAGCGTGAGGATGATAAAC
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                                                                                ATTACAACAAAGGTGTCTTGAAAAACATTGATGGTTCAAAA 618
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Pred. No. 5.9e-15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 7.3%;
Best Local Similarity 47.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                            10982 TGATTATGGGCTTACCTGGTGCAGGTAAGGGAACTCAAGCAGCAAAAATCGTAGAACAAT 11041
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
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TITLE OF INVENTION: Strep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION: TELEPHONE: (301) 309-8504 TELEFAX: (301) 309-8512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 424
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                      316
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                                                                                                                                     368
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 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 11831 base pairs TYPE: nucleic acid STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: HP Vect
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Brookes, A. Ander: REGISTRATION NUMBER: 36. REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET:
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                                                                                                    TTGGCATTGAACTAGAAGGTGTTATCAATATTGAAGTGAACCCTGACAGCCTTTTGGAAC
                                                                                                                                                                                                   CAAATGGAATCGTAAAAGAACGCCTTTCACAAGATGATATTAAAGAAACAGGATTCTTAT 11221
                                                                                                                                                                                                                                                                                                                          AAATTGGCGTGTTAGCCAAGGCTTTCATTGACCAAGGGAAACTCATCCCAGATGATGTCA 261
                                                                                                                                                                                                                                                                                                                                                                         TCCATGTTGCACATATCTCAACAGGTGATATGTTCCGCGCTGCAATGGCAAATCAAACTG 11101
                                                                                                                                                                                                                                                                                                                                                                                                           TCGAGCTGAAGCACCTCTCCAGCGGGGACCTGCTCCGGGACAACATGCTGCGGGGCACAG 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGATCATGGGGGCCCCGGGCTCGGGCAAGGGCACCGTGTCGTCGCGCATCACTACACACT 141
 CTCCCAAAACTGTGGGCATTGATGACCTGACTGGGGAGCCTCTCATTCAGCGTGAGGATG 540
                                   GTTTGAGTGGGCGTATCATCCACCGCGTAACTGGAGAAACTTTCCACAAGGTCTTTAACC
                                                                  GCCTTACTGCTCGCTGGATTCATCCCGCCAGTGGCCGAGTCTATAACATTGAATTCAACC 480
                                                                                                                                  ----TCAGATCGACACAGTGATTAACCTGAATGTGCCCTTTGAGGTCATTAAACAAC 420
                                                                                                                                                                                                                                                                     AAATGGGTGTTCTTGCTAAGTCATATATTGACAAGGGTGAATTGGTTCCTGACGAAGTTA 11161
                                                                                                                                                                     TGGATGGTTACCCACGTACAATTGAACAAGCTCATGCCTTGGACAAAACATTGGCTGAAC 1128:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 308;
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HP Vectra 486/33
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Pred. No. 1.9e-08;
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                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                              Matches 100;
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                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
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ENERAL INFORMATION:
5533 TGGCCCCGGCCCTGCTGACCGTGGGCACCGCGGCGCTGCGCCGGATCACGCCGCTGCGGC
                                                                                                                                                                                                                                   TOPOLOGY: 1
                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 30001 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Fantini, Susan E.
TITLE OF INVENTION: Cloning of the biosynthetic pathway for
TITLE OF INVENTION: chlortetracycline and tetracyline Formation and cosmids
TITLE OF INVENTION: useful therein
                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
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CORRESPONDENCE ADDRESS:
                  136 CACACTTCGAGCTGAAGCACCTCTCCAGCGGGGACCTGCTCCGGGGACAACATGCTGCGGG 195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: FILING DATE: 22-SEI CLASSIFICATION: 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0
                                                                                                                                                                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Tsevdos, Estelle J
REGISTRATION NUMBER: 31,145
REFERENCE/DOCKET NUMBER: 31
                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: US
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                                                                  GGCCGTGCTGCTGCGCTCCACCCGCACGGCCACCGCCCTGGTGTCGCTGCGCACCGCGC 5534
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATAAGCCTGAGACAGTAAAAACGTCGTTTGGATGTTAATATTGCTCAAGGAGAACCAATCA 11506
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Wayne
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                                                                                                                                                                                                                                                                                                                                                           : (201)831-3241
(201)831-3305
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                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                       linear
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                                                                                                                                                                                                                                   DNA (genomic)
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                                                                                                                                                             Score 40; DB 1; Pred. No. 0.15;
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                                                                                                                                          Mismatches
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                                                                                                                                                Query Match
Best Local
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APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 31
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201)831-3241
                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 22-SEP-1993
                                                                5593 GGGCCGTGCTGCGCTCCACCCGCCACGGCCACCGCCCTGGTGTCGCTGCGCACCGCGC
                                                                                                                                                                                                                   MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION NAME: Tsevdos, Estelle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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NUMBER OF SEQUENCES:
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                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                              STRANDEDNESS:
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                                                                                                                                                                                                                                                                                LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
                              CACACTTCGAGCTGAAGCACCTCTCCAGCGGGGACCTGCTCCGGGACAACATGCTGCGGG 195
                                                                                                 GAGCGGTGATCATGGGGGCCCCGGGCTCGGGCAAGGGCACCGTGTCGTCGCGCATCACTA 135
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                                                                                                                                                                                                                                                               nucleic acid
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                                                                                                                                                                                                                 DNA (genomic)
                                                                                                                                                                                                                                                single
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                                                                                                                                                4.7%;
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Pred. No. 0.15;
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                                                                                                                                   Mismatches
                                                                                                                                                                DB 2;
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256 ATGTCATGACTCGGCTGGCC

275

NUMBER OF SEQUENCES:

1120

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US-09-221-017B-913
; Sequence 913, Application US/09221017B
; Patent No. 6444799
; GENERAL INFORMATION:
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Best Local Similarity
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Patent No. 6015890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (212) 286-0854 or 286-0082
TELEX: TWX 710-581-4766
INFORMATION FOR SEQ ID NO: 45:
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TITLE OF INVENTION: MUTANTS THEREOF
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LENGTH: 10095
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ATTORNEY/AGENT INFORMATION:
NAME: ELIZABETH A. BOGOSIAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH 1.44 Mb STORAGE
MEDIUM TYPE: DISKETTE
COMPUTER: IBM PC COMPATIBLE
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HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 697-5995
APPLICANT: ROSS, Bruce C.
TITLE OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                           133 CTACACACTTCGAGCTGAAGCACCTCTCCAGCGGGGACCTGCTCCGGGGACAACATGCT 190
                                                                                                                                                                                                                                                              73 TGCGAGCGGTGATCATGGGGGCCCCGGGCTCGGGGCAAGGGCACCGTGTCGTCGCGCATCA 132
                                                                                                                                                                                                                                                                                                                                                 13 GCCCTGGTACCCGCGCGCGGGGCCTCAGTCTGCGGCCCATGGGGGGCGTCCGCGGCGGCTGC 72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 39,911
REFERENCE/DOCKET NUMBER: 96
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                                                                                                                                                                                                                                         TCACCGTGGTGTTTTCGGGACCAGACGCTGGCCACGGTGGCCGAATCGGCACGCATCA 4973
                                                                                                                                                                                                                                                                                                                                                                                          91;
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90 PARK AVENUE
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                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                      Score 38.8; DB Pred. No. 0.19; O; Mismatches
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRILING DATE: 09-APR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/AL
FILING DATE: 10-DEC-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 32,430
REFERENCE/DOCKET NUMBER: 27
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-813-5600
4311 ACCTGACAGCCTGATCGTGGACATGATGGAAAAGCTCATCAGCACTTTGGTCGATACCGA 4370
                                                                                                                                                                                                     4131 GATGCTTAACGTACTAATCTTCGGTGCTCCCGGTTCCGGGAAGGCCACCCAAAGCGAAGA 4190
                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 4530 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PP2911
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                                                                                                                                   4191 ACTGATCCGTCGATATGGATTCCGGCATATTTCAACCGGAGAGTTGCTTCGTGCCGAAAT
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HYPOTHETICAL:
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                                                                                                                                                                 128 CATCACTACACACTTCGAGCTGAAGCACCTCTCCAGCGGGGACCTGCTCCGGGGACAACAT 187
                                                                                                                                                                                                                                                                                                                                                                                                                                           ANTI-SENSE:
                               248 CCCAGATGATGTCATGACTCGGCTGGCCCTTCATGAGCTGAAAAATCTCACCCA---GTA 304
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                                                                                                                                                                                                                                     68 GCTGCTGCGAGCGGTGATCATGGGGGGCCCCGGGCTCGGGCAAGGGCACCGTGTCGTCGCG 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: PP29.
FTLING DATE: 09-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: FILING DATE: 30-JAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: PP11 FILING DATE: 31-DEC-1997
                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature
LOCATION: 1...4530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS: doub! TOPOLOGY: circular
                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: FILING DATE: 23-DE
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                                                                                                 GCTGCGGGGCACAGAAATTGGCGTGTTAGCCAAGGCTTTCATTGACCAAGGGAAACTCAT 247
                                                                                                                                                                                                                                                                        142;
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755 PAGE MILL ROAD
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30-JAN-1998
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3ER: 27340-20021.00
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; LENGTH: 3001
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-387-212-9
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US-09-948-802-9
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TITLE OF INVENTION:
TITLE OF INVENTION:
FILE REFERENCE: MNI:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 9, Application US/09387212A Patent No. 6309849 GENERAL INFORMATION:
                                                                                                                                      Query Match 4.4%;
Best Local Similarity 57.0%;
                                                                                                                                                                                                                                               SEQ ID NO 9
                                                                                                                        Matches
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TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN KINASE AND
TITLE OF INVENTION: PHOSPHATASE HOMOLOGUES AND USES THEREFOR
FILE REFERENCE: MNI-090
                                                                                                                                                                                                                                                            PRIOR FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/387,212A
CURRENT FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 18
                                                                                                                                                                                                                                                                                                      CURRENT FILING DATE: 2001-09-07
PRIOR APPLICATION NUMBER: 09/387,212
                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/948,802 CURRENT FILING DATE: 2001-09-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE:
                                                                                                                                                                                                TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                               LENGTH: 3001
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265 CATCGTCGAGAAATATGGCTACACACACCTTTCTGCAGGAGAGCTGCTTCGTGATGAAAG 324
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                                                                                            83
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                                                           GCCGCTGGTCGTCTTCGTCCTCGGCGCGCCCGGCGCAAGGGGACCCAGTGCGCCCG 264
                                                                                       GCTGCTGCGAGCGGTGATCATGGGGGGCCCCGGGCTCGGGCAAGGGCACCGTGTCGTCGCG 127
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                                                                                                                        Conservative
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NUCLEIC ACID MOLECULES
PHOSPHATASE HOMOLOGUES
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57.08;
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Pred. No. 0.19;
0; Mismatches 52;
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US-08-232-463-14
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US-08-232-463-14/c
                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                           Query Match
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Patent No. 5670367
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION: TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                   IMMEDIATE SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
666 CCCTATGTATATGCTTTCCTACAAACTAAAGTTCCACAAAAGAAGCCAGAAAGCTTCAGTT 725
                                                                                                                                                                                                                          486 AAAACTGTGGGCATTGATGACCTGACTGGGGAGCCTCTCATTCAGCGTGAGGATGATAAA 545
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                                                                                                                                                      NAME: BENT, Stephen A. REGISTRATION NUMBER: 29, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
ZIP: 22313-0299
                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE:
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                                                                                                                                                                                                                                                        Local Similarity es 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH:
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                                                                                   TATTACCAGAAAAAAGGGGTGCTGGAAACATTCTCCGGAACAGAAACCAACAAGATTTGG 665
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1800 Diagonal Road,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SCHEIFLINGER, F.
FALKNER, F. G.
WENTION: RECOMBINANT FOWLPOX VIRUS
                                                                                                                                                                                                                                                           Conservative 164;
                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                                                                                                                single
                                                                                                                                                                                                                                                      4.4%; Score 37.2; DB 1;
4.0%; Pred. No. 0.48;
vative 164; Mismatches 124;
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RESULT 13
5244792-1/c
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; APPLICANT: BURKE, RAE L.;PACHL, CAROL;VALENZUELA, PABLO D.T.
TITLE OF INVENTION: EXPRESSION OF RECOMBINANT GLYOPROTEIN
;B FROM HERPES SIMPLEX VIRUS
; NUMBER OF SEQUENCES: 19
; CURRENT APPLICATION DATA:
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                                 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/822,586
FILING DATE: MARCH 20, 1997
ATTORNEY/AGENT INFORMATION:

NAME: ELIZABETH A BOCCOTTOR
                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH
MEDIUM TYPE: DISKETTE
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APPLICATION NUMBER: 921,730
FILING DATE: 20-0CT-1986
APPLICATION NUMBER: 597,784
                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: AMSTER, F
                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: WIILIAM R. JACOBS, JR., JAMES M. MUSSER AND APPLICANT: AMALIO TELENTI TITLE OF INVENTION: AN EMBCAB OPERON OF MYCOBACTERIA AND TITLE OF INVENTION: MUTANTS THEREOF
                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           340 ACCAGCGCGCAAATCAAGCCCCCC 317
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: MS-DOS SOFTWARE: ASCII
                                                                                                                                                                                                                                                                                       CITY: NEW YORK STATE: NEW YOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     78 GCGGTGATCATGGGGGCCCCGGGCTCGGGCAAGGGCACCGTGTCGTCGCGCATCACTACA 137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/587,179 FILING DATE: 20-SEP-1990
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                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 53.5 es 77; Conservative
 REFERENCE/DOCKET NUMBER:
                     REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
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                                                                                                                                                                                                                                                                                     NEW YORK
                                                                                                                                                                                                                                                                                                                          90 PARK AVENUE
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                                                                                                                                                                                                        .5 INCH 1.44 Mb STORAGE
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96700/437
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Search completed: March 19, 2003, 13:35:56
Job time: 166 secs
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Best Local Similarity
Matches 87; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Ver. SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3, Application US/09257541B Patent No. 6198020
                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Bowen, Benjamin A.
APPLICANT: Duvick, Jonathan P.
APPLICANT: Simmons, Carl R.
APPLICANT: Simmons, Carl R.
TITLE OF INVENTION: Nitric Oxide As An Activator Of The Plant Pathogen
TITLE OF INVENTION: Defense Systems
FILE REFERENCE: 5718-35 , 035718/175173
CURRENT APPLICATION NUMBER: US/09/257,541B
CURRENT FILING DATE: 1999-02-24
EARLIER APPLICATION NUMBER: 60/076,153
EARLIER FILING DATE: 1998-02-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 697-5995
TELEFAX: (212) 286-0854 or 286-0082
TELEX: TWX 710-581-4766
INFORMATION FOR SEQ ID NO: 46:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 2098
TYPE: DNA
ORGANISM: Zea mays
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LENGTH: 9960
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4803 TCGCGGCGTCGGTCGTCGTGTCTTCGTGATCATCTTCCGCGATCAGACCCTGGCCACGG 4862
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                                                                                                                                                                                                                                           1145 CTGCAGAGTGAGGTCGCCGCACGCGGCCGCGCGTCGGCCGGGGACAGGTTGCCGCCGCCGCCGC 1086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               112 GCACCGTGTCGCGCGCATCACTACACACTTCGAGCTGAAGCACCTCTCCAGCGGGGACC 171
                                                                                                                                                                                                   83 GATCATGGGGGCCCCGGGCTCGGGCAAGGGCACCGTGTCGTCGCGCATCACTACACACTT 142
                                                                                                                                                                                                                                                                                   23 CCGCGCGGTGGGGCCTCAGTCTGCGGCCCATGGGGGCGTCCGCGGCGGCTGCTGCGAGCGGT 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  52 TGGGGGCGTCCGCGGCTGCTGCGAGCGGTGATCATGGGGGGCCCCGGGCTCGGGCAAGG 111
                                                                                                                                                                                                                                                                                                                                              Local
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                                                                                                  CGAGCTGAAGCACCTCTCCAGCGGGGACCTGCTCCGGGACAACATGCT 190
                                                                                                                                                             GTTGCAGATGGACCCGGCGACGACCACCGCCACGTTGATGAGGAACGCCACCACGAA 1026
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                                                                               CGCCAGGCTGCACTCCACGAGGAAGTACCTGCACGCGGCCCTGATGCT 978
                                                                                                                                                                                                                                                                                                                             85;
                                                                                                                                                                                                                                                                                                                                            4.18;
Similarity 50.68;
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                                                                                                                                                                                                                                                                                                                                            Score 35.2; DB Pred. No. 0.98;
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                                                                                                                                                                                                                                                                                                                           83;
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